

APPLICANT: Ruoslahti, Erkki
APPLICANT: Koivunen, Erkki
TITLE OF INVENTION: No. 5991478e1 Integrin-Binding Peptides
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,861
FILING DATE: 04-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: circular
US-08-286-861-7

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 15
US-08-924-002-1
Sequence 1, Application US/08924002
Patent No. 6177542
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki I.
APPLICANT: Koivunen, Erkki
TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,002
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/625,695

FILING DATE: 03-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,186
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 2748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-924-002-1

Query Match 100.0%; Score 35; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

Search completed: September 22, 2004, 07:02:53
Job time : 34 secs

; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,238
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9775
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-425-238-4

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 12
US-08-625-695A-1
; Sequence 1, Application US/08625695A
; Patent No. 5912234
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki I.
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,695A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,186
; FILING DATE: 11-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 2041
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; US-08-625-695A-1

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 13
US-08-625-695A-26
; Sequence 26, Application US/08625695A
; Patent No. 5912234
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki I.
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,695A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,186
; FILING DATE: 11-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 2041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-625-695A-26

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 14
US-08-286-861-7
; Sequence 7, Application US/08286861
; Patent No. 5981478
; GENERAL INFORMATION:

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Koivunen, Erkki I.
FILING DATE: 11-MAR-1994
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/625,695
FILING DATE: 03-APR-1996
PRIOR APPLICATION DATA:
APPLICANT: Koivunen, Erkki I.
FILING DATE: 11-MAR-1994
TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Koivunen, Erkki I.
FILING DATE: 11-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 2748
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-924-002-10

Query Match 100.0%; Score 35; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
DB 1 CRGDC 5

RESULT 9
US-08-212-186A-1
Sequence 1, Application US/08212186A
Patent No. 5536814
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki I.
APPLICANT: Koivunen, Erkki
TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Koivunen, Erkki
FILING DATE: 11-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9861
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-212-186A-1

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
DB 1 CRGDC 5

RESULT 10
US-08-212-186A-26
Sequence 26, Application US/08212186A
Patent No. 5536814
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki I.
APPLICANT: Koivunen, Erkki
TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Koivunen, Erkki
FILING DATE: 11-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9861
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-212-186A-26

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
DB 1 CRGDC 5

RESULT 11
US-08-425-238-4
Sequence 4, Application US/08425238
Patent No. 5627263
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Koivunen, Erkki
TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California

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Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 5
US-08-753-781-35
; Sequence 35, Application US/08753781C
; Patent No. 5951981
; GENERAL INFORMATION:
; APPLICANT: Markland Jr., Francis S.
; APPLICANT: Bush, Larry R.
; APPLICANT: Swenson, Stephen
; APPLICANT: Flores Sanchez, Eladio
; TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
; FILE REFERENCE: DITI 124
; CURRENT APPLICATION NUMBER: US/08/753,781C
; CURRENT FILING DATE: 1996-12-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-08-753-781-35

Query Match 100.0%; Score 35; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 6
US-08-286-861-37
; Sequence 37, Application US/08286861
; Patent No. 5981478
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,861
; FILING DATE: 04-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

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; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-08-286-861-37

Query Match 100.0%; Score 35; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 7
US-09-141-127-15
; Sequence 15, Application US/09141127A
; Patent No. 6083481
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: THROMBUS IMAGING AGENTS
; FILE REFERENCE: DITI 113.1USC1
; CURRENT APPLICATION NUMBER: US/09/141,127A
; EARLIER FILING DATE: 1998-08-27
; EARLIER APPLICATION NUMBER: 08/335,832
; EARLIER FILING DATE: 1995-01-05
; EARLIER APPLICATION NUMBER: PCT/US93/04794
; EARLIER FILING DATE: 1993-05-21
; EARLIER APPLICATION NUMBER: 07/886,752
; EARLIER FILING DATE: 1992-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-09-141-127-15

Query Match 100.0%; Score 35; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 8
US-08-924-002-10
; Sequence 10, Application US/08924002
; Patent No. 6177542
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki I.
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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Sequence 8, Application US/08425238
 Patent No. 5627263
 GENERAL INFORMATION:
 APPLICANT: Ruoslahti, Erkki
 APPLICANT: Koivunen, Erkki
 TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESS: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/425,238
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/158,001
 FILING DATE: 24-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 9775
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-425-238-8

Query Match 100.0%; Score 35; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 3
 US-08-625-695A-10
 Sequence 10, Application US/08625695A
 Patent No. 5912234
 GENERAL INFORMATION:
 APPLICANT: Ruoslahti, Erkki I.
 APPLICANT: Koivunen, Erkki
 TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CAMPBELL & FLORES, LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/625,695A

FILING DATE: 03-APR-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/212,186
 FILING DATE: 11-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 2041
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: both
 US-08-625-695A-10

Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 4
 US-08-335-832-42
 Sequence 42, Application US/08335832
 Patent No. 5925331
 GENERAL INFORMATION:
 APPLICANT: Dean, Richard T
 APPLICANT: Lister-James, John
 TITLE OF INVENTION: Technetium-99m Labeled Peptides for
 TITLE OF INVENTION: Thrombus Imaging
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Banner & Allegretti, Ltd.
 STREET: 10 South Wacker Drive Suite 3000
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/335,832
 FILING DATE: 05-JAN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5925331nan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 92,216-I
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEFAX: 312-715-1234
 TELEX: 910-221-5317
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-335-832-42

Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: September 22, 2004, 06:51:52 ; Search time 32 Seconds
(without alignments)
8.067 Million cell updates/sec

Title: US-09-912-609-9

Perfect score: 35

Sequence: 1 CRGDC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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3: /cgn2_6/prodata/2/iaa/6A COMB.pep:*
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6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	35	100.0	5	1	US-08-425-238-8
3	35	100.0	5	2	US-08-625-695A-10
4	35	100.0	5	2	US-08-335-832-42
5	35	100.0	5	2	US-08-753-781-35
6	35	100.0	5	2	US-08-286-861-37
7	35	100.0	5	3	US-09-141-127-15
8	35	100.0	5	3	US-08-924-002-10
9	35	100.0	6	1	US-08-212-186A-1
10	35	100.0	6	1	US-08-212-186A-26
11	35	100.0	6	2	US-08-625-695A-1
12	35	100.0	6	2	US-08-425-238-4
13	35	100.0	6	2	US-08-625-695A-26
14	35	100.0	6	2	US-08-286-861-7
15	35	100.0	6	3	US-08-924-002-1
16	35	100.0	6	3	US-08-924-002-1
17	35	100.0	7	3	US-09-026-633-4
18	35	100.0	8	3	US-09-426-680-11
19	35	100.0	9	2	US-08-701-124-3
20	35	100.0	9	2	US-08-701-124-4
21	35	100.0	9	2	US-08-286-861-15
22	35	100.0	9	2	US-08-286-861-15
23	35	100.0	9	2	US-08-286-861-16
24	35	100.0	9	2	US-08-286-861-17
25	35	100.0	9	2	US-08-286-861-18
26	35	100.0	9	2	US-08-286-861-33
27	35	100.0	9	3	US-09-026-633-1
			9	3	US-09-130-225-3

28 35 100.0 9 3 US-09-130-225-4
29 35 100.0 9 3 US-09-124-671-33
30 35 100.0 9 3 US-09-258-754-211
31 35 100.0 9 3 US-09-139-802-1
32 35 100.0 9 3 US-09-042-107-211
33 35 100.0 9 3 US-09-320-424-20
34 35 100.0 9 3 US-09-426-680-12
35 35 100.0 9 4 US-09-455-061-3
36 35 100.0 9 4 US-09-455-061-4
37 35 100.0 9 4 US-08-174-943-8
38 35 100.0 9 4 US-08-315-127-18
39 35 100.0 9 4 US-09-659-786-1
40 35 100.0 9 4 US-09-825-563-20
41 35 100.0 9 4 US-08-926-914-1
42 35 100.0 9 4 US-09-722-2500-211
43 35 100.0 9 4 US-09-969-192-3
44 35 100.0 9 4 US-09-969-192-4
45 35 100.0 9 4 US-09-428-082B-449

ALIGNMENTS

RESULT 1
US-08-212-186A-10
; Sequence 10, Application US/08212186A
; Patent No. 5536914
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki I.
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,186A
; FILING DATE: 11-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9861
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: both
US-08-212-186A-10

Query Match 100.0%; Score 35; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5

Db 1 CRGDC 5

RESULT 2

US-08-425-238-8

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Alanine is attached to DSPE-PEG5k-succinyl
US-10-850-873-10
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Query Match          100.0%; Score 35; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 CRGDC 5
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Db       4 CRGDC 8
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Search completed: September 22, 2004, 07:04:03
Job time : 66 secs
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; PRIOR APPLICATION NUMBER: US 09/801,485
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RGD Peptide
US-10-917-709-2

Query Match 100.0%; Score 35; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 3 CRGDC 7

RESULT 12
US-10-712-298-20
; Sequence 20, Application US/10712298
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/712,298
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: peptide
US-10-712-298-20

Query Match 100.0%; Score 35; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 3 CRGDC 7

RESULT 13
US-10-808-758-78
; Sequence 78, Application US/10808758
; GENERAL INFORMATION:
; APPLICANT: Von Seggern, Daniel J.
; TITLE OF INVENTION: ADENOVIRUS PARTICLES WITH ENHANCED INFECTIVITY OF DENDRITIC CELLS
; FILE REFERENCE: 22908-1239

; CURRENT APPLICATION NUMBER: US/10/808,758
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/459,000
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/467,500
; PRIOR FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CRGD peptide
US-10-808-758-78

Query Match 100.0%; Score 35; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 4 CRGDC 8

RESULT 14
US-09-791-524A-14
; Sequence 14, Application US/09791524A
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc. For Delivery Of Heterologous Genes
; TITLE OF INVENTION: Targeted Adenovirus Vectors
; FILE REFERENCE: P26,992-B USA
; CURRENT APPLICATION NUMBER: US/09/791,524A
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/IB99/01524
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/098,028
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524A-14

Query Match 100.0%; Score 35; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 4 CRGDC 8

RESULT 15
US-10-850-873-10
; Sequence 10, Application US/10850873
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; FILE REFERENCE: 226272005300
; CURRENT APPLICATION NUMBER: US/10/850,873
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/10/136,187
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/287,786
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45

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; Sequence 4, Application US/10729156
; GENERAL INFORMATION:
; APPLICANT: Wang, Shaomeng
; APPLICANT: Yang, Dajun
; TITLE OF INVENTION: Small Molecule Antagonists of BCL-2 Family Proteins
; FILE REFERENCE: UM-08477
; CURRENT APPLICATION NUMBER: US/10/729,156
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-729-156-4

Query Match      100.0%; Score 35; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDC 5
Db      3 CRGDC 7

RESULT 8
US-10-877-930-33
; Sequence 33, Application US/10877930
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: alpha-five integrin binding motif
US-10-877-930-33

Query Match      100.0%; Score 35; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDC 5
Db      3 CRGDC 7

RESULT 9
US-10-900-399-20
; Sequence 20, Application US/10900399
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/900,399
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US/09/320,424
; PRIOR FILING DATE: 1999-05-26

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; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: peptide
US-10-900-399-20

Query Match      100.0%; Score 35; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDC 5
Db      3 CRGDC 7

RESULT 10
US-10-912-764-34
; Sequence 34, Application US/10912764
; GENERAL INFORMATION:
; APPLICANT: SHEN, BEN
; TITLE OF INVENTION: TARGETED CARRIER FUSIONS FOR DELIVERY OF
; FILE REFERENCE: WARF.011US
; CURRENT APPLICATION NUMBER: US/10/912,764
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: 60/492,508
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-912-764-34

Query Match      100.0%; Score 35; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDC 5
Db      3 CRGDC 7

RESULT 11
US-10-917-709-2
; Sequence 2, Application US/10917709
; GENERAL INFORMATION:
; APPLICANT: Dickerson, Erin B.
; APPLICANT: Helfand, Stuart C.
; APPLICANT: Akhtar, Nasim
; TITLE OF INVENTION: METHODS FOR TARGETING INTERLEUKIN-12 TO MALIGNANT ENDOTHELIUM
; FILE REFERENCE: WARF-0025
; CURRENT APPLICATION NUMBER: US/10/917,709
; CURRENT FILING DATE: 2004-08-13

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PCT-US04-16382-7

Query Match 100.0%; Score 35; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 3 CRGDC 7

RESULT 3

US-09-612-852A-14
; Sequence 14, Application US/09612852A
; GENERAL INFORMATION:
; APPLICANT: KRASNYKH, VICTOR N.
; TITLE OF INVENTION: MODIFIED ADENOVIRUS CONTAINING A FIBER REPLACEMENT PROTEIN
; FILE REFERENCE: 678503-2006.2
; CURRENT APPLICATION NUMBER: US/09/612,852A
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/250,580
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/074,844
; PRIOR FILING DATE: 1998-02-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Peptide ligand
; OTHER INFORMATION: containing the RGD motif

US-09-612-852A-14

Query Match 100.0%; Score 35; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 3 CRGDC 7

RESULT 4

US-09-791-524A-124
; Sequence 124, Application US/09791524A
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
; FILE REFERENCE: P26,992-B USA
; CURRENT APPLICATION NUMBER: US/09/791,524A
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/IB99/01524
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/098,028
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Adenovirus
; OTHER INFORMATION: alpha-five integrin binding motif

US-09-791-524A-124

Query Match 100.0%; Score 35; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 3 CRGDC 7

RESULT 5

US-10-342-081-76
; Sequence 76, Application US/10342081
; GENERAL INFORMATION:
; APPLICANT: Rajopadhye, Milind
; APPLICANT: Edwards, D. Scott
; APPLICANT: Barrett, John A.
; APPLICANT: Carpenter, Jr., Alan P.
; APPLICANT: Hartis, Thomas D.
; APPLICANT: Heminway, Stuart J.
; APPLICANT: Liu, Shuang
; APPLICANT: Singh, Prahlad R.
; TITLE OF INVENTION: PHARMACEUTICALS FOR THE IMAGING OF ANGIOGENIC DISORDERS
; FILE REFERENCE: BMS-2024
; CURRENT APPLICATION NUMBER: US/10/342,081
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 09/599,295
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct

US-10-342-081-76

Query Match 100.0%; Score 35; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 3 CRGDC 7

RESULT 6

US-10-815-514-33
; Sequence 33, Application US/10815514
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/815,514
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/696,872
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: alpha-five integrin binding motif

US-10-815-514-33

Query Match 100.0%; Score 35; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 3 CRGDC 7

RESULT 7

US-10-729-156-4

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2004, 06:52:17 ; Search time 64 Seconds
(without alignments)
10.631 Million cell updates/sec

Title: US-09-912-609-9
Perfect score: 35
Sequence: 1 CRGDC 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 735861 seqs, 136079791 residues

Total number of hits satisfying chosen parameters: 735861

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Pending Patents AA New:*
- 1: /cgn2_6/ptodata/1/paa/PCT NEW COMB.pep.*
 - 2: /cgn2_6/ptodata/1/paa/US06 NEW COMB.pep.*
 - 3: /cgn2_6/ptodata/1/paa/US07 NEW COMB.pep.*
 - 4: /cgn2_6/ptodata/1/paa/US08 NEW COMB.pep.*
 - 5: /cgn2_6/ptodata/1/paa/US09 NEW COMB.pep.*
 - 6: /cgn2_6/ptodata/1/paa/US10 NEW COMB.pep.*
 - 7: /cgn2_6/ptodata/1/paa/US60 NEW COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	7	5	US-09-791-524A-148
2	35	100.0	9	1	PCT-US04-16382-7
3	35	100.0	9	5	US-09-612-852A-14
4	35	100.0	9	5	US-09-791-524A-124
5	35	100.0	9	6	US-10-342-081-76
6	35	100.0	9	6	US-10-815-514-33
7	35	100.0	9	6	US-10-729-156-4
8	35	100.0	9	6	US-10-877-930-33
9	35	100.0	9	6	US-10-900-399-20
10	35	100.0	9	6	US-10-912-764-34
11	35	100.0	9	6	US-10-917-709-2
12	35	100.0	9	6	US-10-712-298-20
13	35	100.0	10	6	US-10-808-758-78
14	35	100.0	11	5	US-09-791-524A-14
15	35	100.0	11	6	US-10-850-873-10
16	35	100.0	11	6	US-10-850-873-14
17	35	100.0	11	6	US-10-469-131-27
18	35	100.0	11	6	US-10-912-764-35
19	35	100.0	11	6	US-10-917-709-1
20	35	100.0	12	6	US-10-627-649-282
21	35	100.0	12	6	US-10-627-649-315
22	35	100.0	12	6	US-10-627-649-316
23	35	100.0	13	5	US-09-791-524A-13
24	35	100.0	13	5	US-09-791-524A-23
25	35	100.0	15	5	US-09-791-524A-22
26	35	100.0	16	6	US-10-917-709-10

27	35	100.0	18	6	US-10-917-709-8	Sequence 8, Appli
28	35	100.0	18	6	US-10-917-709-9	Sequence 9, Appli
29	35	100.0	24	6	US-10-627-649-281	Sequence 281, App
30	35	100.0	24	6	US-10-627-649-283	Sequence 283, App
31	35	100.0	24	6	US-10-627-649-301	Sequence 301, App
32	35	100.0	24	6	US-10-627-649-302	Sequence 302, App
33	35	100.0	25	6	US-10-627-649-311	Sequence 311, App
34	35	100.0	25	6	US-10-627-649-312	Sequence 312, App
35	35	100.0	25	6	US-10-627-649-313	Sequence 313, App
36	35	100.0	25	6	US-10-627-649-314	Sequence 314, App
37	35	100.0	49	6	US-10-767-701-50090	Sequence 50090, A
38	35	100.0	214	6	US-10-425-115-336322	Sequence 336322,
39	35	100.0	214	6	US-10-425-115-336324	Sequence 336324,
40	35	100.0	332	6	US-10-808-758-20	Sequence 20, Appl
41	35	100.0	363	6	US-10-425-115-321051	Sequence 321051,
42	35	100.0	397	6	US-10-808-758-24	Sequence 24, Appl
43	35	100.0	582	6	US-10-808-758-6	Sequence 6, Appli
44	35	100.0	582	6	US-10-808-758-12	Sequence 12, Appl
45	35	100.0	591	6	US-10-808-758-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-791-524A-148
; Sequence 148, Application US/09791524A
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
; FILE REFERENCE: P26,992-B USA
; CURRENT APPLICATION NUMBER: US/09/791.524A
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/IB99/01524
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/098,028
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524A-148

Query Match Similarity 100.0%; Score 35; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.5e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 CRGDC 5
Db 2 CRGDC 6

RESULT 2
PCT-US04-16382-7
; Sequence 7, Application PC/TUS0416382
; GENERAL INFORMATION:
; APPLICANT: MOUNT SINAI SCHOOL OF MEDICINE OF NEW YORK UNIVERSITY
; APPLICANT: WEBER, Thomas
; APPLICANT: GIGOUT, Laure
; TITLE OF INVENTION: VIRAL VECTORS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 02420/200M817-WO0
; CURRENT APPLICATION NUMBER: PCT/US04/16382
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: peptide ligand

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 14

US-07-961-889-92
; Sequence 92, Application US/07961889
; GENERAL INFORMATION:
; APPLICANT: Lobl, Thomas J.
; APPLICANT: Chiang, Shiu-Lan
; APPLICANT: Cardarelli, Pina M.
; TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Fifth Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/961,889
; FILING DATE: 04-JUN-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/550,330
; FILING DATE: 09-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Bostlich, June M.
; REGISTRATION NUMBER: 31,238
; REFERENCE/DOCKET NUMBER: Tanabe #7126/PD1381
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue 1 is
; OTHER INFORMATION: 1-adamantanecetic acid."
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 2..6
US-07-961-889-92

Query Match 100.0%; Score 35; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 2 CRGDC 6

RESULT 15

US-08-575-461-92
; Sequence 92, Application US/08575461
; GENERAL INFORMATION:
; APPLICANT: Lobl, Thomas J.
; APPLICANT: Chiang, Shiu-Lan
; APPLICANT: Cardarelli, Pina M.

; TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Fifth Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,461
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/961,889
; FILING DATE: 04-JUN-1993
; APPLICATION NUMBER: US 07/550,330
; FILING DATE: 09-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Bostlich, June M.
; REGISTRATION NUMBER: 31,238
; REFERENCE/DOCKET NUMBER: Tanabe #7126/PD1381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue 1 is
; OTHER INFORMATION: 1-adamantanecetic acid."
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 2..6
US-08-575-461-92

Query Match 100.0%; Score 35; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 2 CRGDC 6

Search completed: September 22, 2004, 07:02:14
Job time : 431 secs

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; Sequence 9, Application US/09912609
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: MATSUNAGA, TERRY ONICHI
; APPLICANT: ROMANOWSKI, MAREK J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 5030-0001.24
; CURRENT APPLICATION NUMBER: US/09/912,609
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/478,124
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-912-609-9

Query Match      100.0%; Score 35; DB 24; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 11
US-10-304-160-2
; Sequence 2, Application US/10304160
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J
; APPLICANT: KOVESDI, IMRE
; APPLICANT: ROELVINK, PETRUS W
; APPLICANT: EINFELD, DAVID
; APPLICANT: BROUGH, DOUGLAS E
; APPLICANT: LIZONOVA, ALENA
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TARGETING AN ADENOVIRAL VECTOR
; FILE REFERENCE: 220148
; CURRENT APPLICATION NUMBER: US/10/304,160
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: PCT/US01/17391
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 09/631,191
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 60/208451
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-304-160-2

Query Match      100.0%; Score 35; DB 29; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 12
US-60-208-451-2
; Sequence 2, Application US/60208451
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J
; APPLICANT: Kovesdi, Imre
; APPLICANT: Roelvink, Petrus W
; APPLICANT: Einfeld, David
; APPLICANT: Brough, Douglas E
; APPLICANT: Lizonova, Alena
; TITLE OF INVENTION: ALTERNATIVELY TARGETED ADENOVIRUS
; FILE REFERENCE: 205046
; CURRENT APPLICATION NUMBER: US/60/208,451
; CURRENT FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-208-451-2

Query Match      100.0%; Score 35; DB 33; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 13
PCT-US94-13542-7
; Sequence 7, Application PC/TUS9413542
; GENERAL INFORMATION:
; APPLICANT: La Jolla Cancer Research Foundation
; TITLE OF INVENTION: Novel Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13542
; FILING DATE: 22-NOV-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hook, Gregory
; REGISTRATION NUMBER: 38,701
; REFERENCE/DOCKET NUMBER: FP-LA 1220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
PCT-US94-13542-7

Query Match      100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 7
US-09-364-597A-37
Sequence 37, Application US/09364597A
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
TITLE OF INVENTION: Novel Integrin-Binding Peptides
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,597A
FILING DATE: 30-JUL-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,861
FILING DATE: 04-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 3419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 535-9001
TELEFAX: (858) 535-8949
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: circular
US-09-364-597A-37

Query Match 100.0%; Score 35; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 8
US-09-627-035-10
Sequence 10, Application US/09627035
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki I.
TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/627,035
FILING DATE: 27-Jul-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/212,186
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9861
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: both
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-627-035-10

Query Match 100.0%; Score 35; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 9
US-09-699-679A-24
Sequence 24, Application US/09699679A
GENERAL INFORMATION:
APPLICANT: Unger, Evan C.
APPLICANT: Shen, Dekang
APPLICANT: Wu, Guanli
TITLE OF INVENTION: Novel Targeted Compositions For Diagnostics And Therapeutic Use
FILE REFERENCE: UNGR1598
CURRENT APPLICATION NUMBER: US/09/699,679A
CURRENT FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 09/218,660
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 08/660,032
PRIOR FILING DATE: 1996-06-06
PRIOR APPLICATION NUMBER: 08/640,464
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/497,684
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent in version 3.2
SEQ ID NO 24
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-09-699-679A-24

Query Match 100.0%; Score 35; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 10
US-09-912-609-9

;/ TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
;/ NUMBER OF SEQUENCES: 25
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Campbell and Flores
;/ STREET: 4370 La Jolla Village Drive, Suite 700
;/ CITY: San Diego
;/ STATE: California
;/ COUNTRY: USA
;/ ZIP: 92122
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/625,695
;/ FILING DATE:
;/ CLASSIFICATION: 514
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Campbell, Cathryn A.
;/ REGISTRATION NUMBER: 31,815
;/ REFERENCE/DOCKET NUMBER: P-LA 9861
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (619) 535-9001
;/ TELEFAX: (619) 535-8949
;/ INFORMATION FOR SEQ ID NO: 10:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 5 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: both
;/ MOLECULE TYPE: peptide
;/ US-08-625-695-10

Query Match 100.0%; Score 35; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 5
US-08-753-781B-45
;/ Sequence 45, Application US/08/753781B
;/ GENERAL INFORMATION:
;/ APPLICANT: Markland, Francis S
;/ APPLICANT: Bush, Larry R
;/ APPLICANT: Swenson, Stephen
;/ APPLICANT: Sanchez, Eladio F
;/ TITLE OF INVENTION: Thrombolytic Agents with Antithrombotic
;/ TITLE OF INVENTION: Properties
;/ NUMBER OF SEQUENCES: 54
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
;/ STREET: 300 South Wacker Drive
;/ CITY: Chicago
;/ STATE: Illinois
;/ COUNTRY: USA
;/ ZIP: 60606
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/753,781B
;/ FILING DATE: 02-DEC-1996
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Noonan, Kevin E
;/ REGISTRATION NUMBER: 35,303
;/ REFERENCE/DOCKET NUMBER: 96,2056
;/ TELECOMMUNICATION INFORMATION:

;/ TELEPHONE: 312 913 0001
;/ TELEFAX: 312 913 0002
;/ TELEX:
;/ INFORMATION FOR SEQ ID NO: 45:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 5 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-753-781B-45

Query Match 100.0%; Score 35; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 6
US-08-982-981-45
;/ Sequence 45, Application US/08982981
;/ GENERAL INFORMATION:
;/ APPLICANT: Markland Jr., Francis S.
;/ APPLICANT: Bush, Larry R.
;/ APPLICANT: Swenson, Stephen
;/ APPLICANT: Flores Sanchez, Eladio
;/ TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC
;/ TITLE OF INVENTION: ACTIVITY
;/ NUMBER OF SEQUENCES: 54
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Diatide, Inc.
;/ STREET: 9 Delta Drive
;/ CITY: Londonderry
;/ STATE: NH
;/ COUNTRY: USA
;/ ZIP: 03053
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/982,981
;/ FILING DATE:
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/753,781
;/ FILING DATE: 02-DEC-1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: McDaniels, Patricia A.
;/ REGISTRATION NUMBER: 33,194
;/ REFERENCE/DOCKET NUMBER: DITI 124.1
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 603 437 8970
;/ TELEFAX: 603 437 8977
;/ INFORMATION FOR SEQ ID NO: 45:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 5 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS:
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-982-981-45

Query Match 100.0%; Score 35; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

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Query Match          100.0%; Score 35; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDC 5
DB      1 CRGDC 5

RESULT 3
US-08-575-461-55
; Sequence 55, Application US/08575461
; GENERAL INFORMATION:
; APPLICANT: Lobl, Thomas J.
; APPLICANT: Chiang, Shiu-Lan
; APPLICANT: Cardarelli, Pina M.
; TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
; TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Fifth Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,461
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/961,889
; FILING DATE: 04-JUN-1993
; APPLICATION NUMBER: US 07/550,330
; FILING DATE: 09-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Bostich, June M.
; REGISTRATION NUMBER: 31,238
; REFERENCE/DOCKET NUMBER: Tanabe #7126/PD1381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 1..5
; US-08-575-461-55

Query Match          100.0%; Score 35; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDC 5
DB      1 CRGDC 5

RESULT 4
US-08-625-695-10
; Sequence 10, Application US/08625695
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki I.
; APPLICANT: Koivunen, Erkki

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2004, 06:49:42 ; Search time 430 Seconds
(without alignments)
11.349 Million cell updates/sec

Title: US-09-912-609-9

Perfect score: 35

Sequence: 1 CRGDC 5

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
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- 19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
- 20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
- 21: /cgn2_6/ptodata/2/paa/US097A_COMB.pep.*
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- 23: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
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- 26: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
- 27: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
- 28: /cgn2_6/ptodata/2/paa/US102_COMB.pep.*
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- 30: /cgn2_6/ptodata/2/paa/US104_COMB.pep.*
- 31: /cgn2_6/ptodata/2/paa/US106_COMB.pep.*
- 32: /cgn2_6/ptodata/2/paa/US107_COMB.pep.*
- 33: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
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RESULT 1
PCT-US94-13542-37
; Sequence 37, Application PC/TUS9413542
; GENERAL INFORMATION:
; APPLICANT: La Jolla Cancer Research Foundation
; TITLE OF INVENTION: Novel Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13542
; FILING DATE: 22-NOV-1994
; CLASSIFICATION:

ALIGNMENTS

Sequence 37, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 10, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 10, Appl
Sequence 37, Appl
Sequence 10, Appl
Sequence 24, Appl
Sequence 9, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 7, Appl
Sequence 92, Appl
Sequence 1, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 26, Appl
Sequence 10, Appl
Sequence 13, Appl
Sequence 148, App
Sequence 4, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 166, App
Sequence 25, Appl
Sequence 9, Appl
Sequence 78, Appl
Sequence 84, Appl
Sequence 102, App
Sequence 1, Appl
Sequence 70, App
Sequence 685, App
Sequence 12, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 33, Appl
Sequence 16, Appl
Sequence 49, App
Sequence 450, App
Sequence 451, App
Sequence 452, App

; TELEPHONE: (858) 535-9001
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; US-09-364-597A-18

Query Match 100.0%; Score 35; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CRGDC 5
|||
Db 3 CRGDC 7

Search completed: September 22, 2004, 07:06:15
Job time : 128 secs

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RESULT 13
US-09-364-597A-16
; Sequence 16, Application US/09364597A
; Patent No. US20020103130A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: No. US20020103130A1 Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,597A
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; APPLICATION DATA:
; FILING DATE: 04-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 535-9001
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; US-09-364-597A-17
;
Query Match 100.0%; Score 35; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 3 CRGDC 7

RESULT 14
US-09-364-597A-17
; Sequence 17, Application US/09364597A
; Patent No. US20020103130A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: No. US20020103130A1 Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,597A
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; APPLICATION DATA:
; FILING DATE: 04-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 535-9001
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; US-09-364-597A-16
;
Query Match 100.0%; Score 35; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 3 CRGDC 7

RESULT 15
US-09-364-597A-18
; Sequence 18, Application US/09364597A
; Patent No. US20020103130A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: No. US20020103130A1 Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,597A
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; APPLICATION DATA:
; FILING DATE: 04-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 535-9001
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; US-09-364-597A-17
;
Query Match 100.0%; Score 35; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 3 CRGDC 7

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; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US/09/765,086
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 09/489,582
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-765-086-1

Query Match 100.0%; Score 35; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
DB 3 CRGDC 7

RESULT 10

US-09-845-160-5
; Sequence 5, Application US/09845160
; Patent No. US20020058045A1
; GENERAL INFORMATION:
; APPLICANT: MIZUGUCHI, HIROYUKI
; APPLICANT: HAYAKAWA, TAKAO
; TITLE OF INVENTION: ADENOVIRUS VECTOR
; FILE REFERENCE: 081356/0163
; CURRENT APPLICATION NUMBER: US/09/845,160
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: JP 2001-131688
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP 2000-161577
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: RGD-4C peptide.

Query Match 100.0%; Score 35; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
DB 3 CRGDC 7

RESULT 11

US-09-245-603A-16
; Sequence 16, Application US/09245603A
; Patent No. US20020081280A1
; GENERAL INFORMATION:
; APPLICANT: Curiel, David T.
; APPLICANT: Krasnykh, Victor N.
; APPLICANT: Dmitriev, Igor
; TITLE OF INVENTION: Adenovirus Vector Containing A Heterologous Peptide
; FILE REFERENCE: D6080
; CURRENT APPLICATION NUMBER: US/09/245,603A
; CURRENT FILING DATE: 1999-02-05

; PRIOR APPLICATION NUMBER: US 60/099,801
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a RGD peptide incorporated
; OTHER INFORMATION: into the region of the fiber gene within the HI loop.
US-09-245-603A-16

Query Match 100.0%; Score 35; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
DB 3 CRGDC 7

RESULT 12

US-09-364-597A-15
; Sequence 15, Application US/09364597A
; Patent No. US20020103130A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: No. US20020103130A1 Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,597A
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,861
; FILING DATE: 04-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 3419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 535-9001
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-364-597A-15

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Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5/
DB 3 CRGDC 7

US-09-912-609-10
 ; Sequence 10, Application US/09912609
 ; Publication No. US20020041898A1
 ; GENERAL INFORMATION:
 ; APPLICANT: UNGER, EVAN C.
 ; APPLICANT: MATSUNAGA, TERRY ONICHI
 ; APPLICANT: RAMASWAMI, VARADARAJAN
 ; APPLICANT: ROMANOWSKI, MAREK J.
 ; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
 ; FILE REFERENCE: 5030-0001.24
 ; CURRENT APPLICATION NUMBER: US/09/912,609
 ; CURRENT FILING DATE: 2001-07-25
 ; PRIOR APPLICATION NUMBER: 09/703,474
 ; PRIOR FILING DATE: 2000-10-31
 ; PRIOR APPLICATION NUMBER: 09/478,124
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 131
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 10
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 US-09-912-609-10

Query Match 100.0%; Score 35; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 6

US-09-912-609-13
 ; Sequence 13, Application US/09912609
 ; Publication No. US20020041898A1
 ; GENERAL INFORMATION:
 ; APPLICANT: UNGER, EVAN C.
 ; APPLICANT: MATSUNAGA, TERRY ONICHI
 ; APPLICANT: RAMASWAMI, VARADARAJAN
 ; APPLICANT: ROMANOWSKI, MAREK J.
 ; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
 ; FILE REFERENCE: 5030-0001.24
 ; CURRENT APPLICATION NUMBER: US/09/912,609
 ; CURRENT FILING DATE: 2001-07-25
 ; PRIOR APPLICATION NUMBER: 09/703,474
 ; PRIOR FILING DATE: 2000-10-31
 ; PRIOR APPLICATION NUMBER: 09/478,124
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 131
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 US-09-912-609-13

Query Match 100.0%; Score 35; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 7
 US-09-791-524-148
 ; Sequence 148, Application US/09791524
 ; Publication No. US20030143209A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aventis Pharmaceuticals Products Inc.
 ; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
 ; FILE REFERENCE: A3319A
 ; CURRENT APPLICATION NUMBER: US/09/791,524
 ; CURRENT FILING DATE: 2001-02-22
 ; PRIOR APPLICATION NUMBER: 60/09828
 ; PRIOR FILING DATE: 1998-08-27
 ; NUMBER OF SEQ ID NOS: 150
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 148
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Adenovirus
 US-09-791-524-148

Query Match 100.0%; Score 35; DB 10; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 2 CRGDC 6

RESULT 8

US-10-013-009-4
 ; Sequence 4, Application US/10013009
 ; Publication No. US20020086815A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McMorris, Trevor C.
 ; APPLICANT: Kelnner, Michael J.
 ; TITLE OF INVENTION: Antitumor agents
 ; FILE REFERENCE: 103.008US3
 ; CURRENT APPLICATION NUMBER: US/10/013,009
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: US 09/386,555
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: US 09/026,633
 ; PRIOR FILING DATE: 1998-02-20
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic amino acid sequence
 US-10-013-009-4

Query Match 100.0%; Score 35; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 Db 2 CRGDC 6

RESULT 9

US-09-765-086-1
 ; Sequence 1, Application US/09765086
 ; Patent No. US20010046498A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; APPLICANT: Pasqualini, Renata
 ; APPLICANT: Wadlin, Arap
 ; APPLICANT: Bredesen, Dale E.
 ; APPLICANT: Ellerby, H. Michael

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; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-364-597A-37

Query Match      100.0%; Score 35; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 2
US-09-912-609-9
; Sequence 9, Application US/09912609
; Publication No. US20020041898A1
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: MATSUNAGA, TERRY ONICHI
; APPLICANT: RAMASWAMI, VARADARAJAN
; APPLICANT: ROMANOWSKI, MAREK J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 5030-0001.24
; CURRENT APPLICATION NUMBER: US/09/912,609
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/478,124
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-912-609-9

Query Match      100.0%; Score 35; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 3
US-10-304-160-2
; Sequence 2, Application US/10304160
; Publication No. US20030099619A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J
; APPLICANT: KOVESDI, IMRE
; APPLICANT: ROELVINK, PETRUS W
; APPLICANT: EINFELD, DAVID
; APPLICANT: BROUGH, DOUGLAS E
; APPLICANT: LIZONOVA, ALENA
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TARGETING AN ADENOVIRAL VECTOR
; FILE REFERENCE: 220148
; CURRENT APPLICATION NUMBER: US/10/304,160
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: PCT/US01/17391
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 09/631,191
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 60/208451

; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-364-597A-7

Query Match      100.0%; Score 35; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 4
US-09-364-597A-7
; Sequence 7, Application US/09364597A
; Patent No. US20020103130A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: NO. US20020103130A1el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,597A
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,861
; FILING DATE: 04-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 3419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 535-9001
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-364-597A-7

Query Match      100.0%; Score 35; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 5
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Title: US-09-912-609-9
Perfect score: 35
Sequence: 1 CRGDC 5
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1342398

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				Query		Description	
Result No.	Score	Match	Length	ID			
1	35	100.0	5	9	US-09-364-597A-37	Sequence 37, Appl	
2	35	100.0	5	12	US-09-912-609-9	Sequence 9, Appl	
3	35	100.0	5	14	US-10-304-160-2	Sequence 2, Appl	
4	35	100.0	6	9	US-09-364-597A-7	Sequence 7, Appl	
5	35	100.0	6	12	US-09-912-609-10	Sequence 10, Appl	
6	35	100.0	6	12	US-09-912-609-13	Sequence 13, Appl	
7	35	100.0	7	10	US-09-912-609-148	Sequence 148, Appl	
8	35	100.0	8	12	US-10-013-009-4	Sequence 4, Appl	
9	35	100.0	9	9	US-09-765-086-1	Sequence 1, Appl	
10	35	100.0	9	9	US-09-845-160-5	Sequence 5, Appl	
11	35	100.0	9	9	US-09-245-603A-16	Sequence 16, Appl	
12	35	100.0	9	9	US-09-364-597A-15	Sequence 15, Appl	
13	35	100.0	9	9	US-09-364-597A-16	Sequence 16, Appl	
14	35	100.0	9	9	US-09-364-597A-17	Sequence 17, Appl	
15	35	100.0	9	9	US-09-364-597A-18	Sequence 18, Appl	

16	35	100.0	9	9	US-09-364-597A-33	Sequence 33, Appl	
17	35	100.0	9	9	US-09-734-628-1	Sequence 1, Appl	
18	35	100.0	9	9	US-09-971-798-5	Sequence 5, Appl	
19	35	100.0	9	9	US-09-969-192-3	Sequence 3, Appl	
20	35	100.0	9	9	US-09-969-192-4	Sequence 4, Appl	
21	35	100.0	9	9	US-09-840-277-14	Sequence 14, Appl	
22	35	100.0	9	9	US-09-840-277-22	Sequence 22, Appl	
23	35	100.0	9	9	US-09-840-277-38	Sequence 38, Appl	
24	35	100.0	9	9	US-09-840-277-62	Sequence 62, Appl	
25	35	100.0	9	9	US-09-840-277-63	Sequence 63, Appl	
26	35	100.0	9	10	US-09-801-485-2	Sequence 2, Appl	
27	35	100.0	9	10	US-09-791-524-124	Sequence 124, Appl	
28	35	100.0	9	12	US-10-609-217-449	Sequence 449, Appl	
29	35	100.0	9	12	US-10-609-217-450	Sequence 450, Appl	
30	35	100.0	9	12	US-10-609-217-451	Sequence 451, Appl	
31	35	100.0	9	12	US-10-609-217-452	Sequence 452, Appl	
32	35	100.0	9	12	US-10-609-217-1076	Sequence 1076, Appl	
33	35	100.0	9	12	US-10-632-388-166	Sequence 166, Appl	
34	35	100.0	9	12	US-10-632-388-449	Sequence 449, Appl	
35	35	100.0	9	12	US-10-632-388-450	Sequence 450, Appl	
36	35	100.0	9	12	US-10-632-388-451	Sequence 451, Appl	
37	35	100.0	9	12	US-10-632-388-452	Sequence 452, Appl	
38	35	100.0	9	12	US-10-632-388-1076	Sequence 1076, Appl	
39	35	100.0	9	12	US-10-651-723-449	Sequence 449, Appl	
40	35	100.0	9	12	US-10-651-723-450	Sequence 450, Appl	
41	35	100.0	9	12	US-10-651-723-451	Sequence 451, Appl	
42	35	100.0	9	12	US-10-651-723-452	Sequence 452, Appl	
43	35	100.0	9	12	US-10-651-723-1076	Sequence 1076, Appl	
44	35	100.0	9	12	US-09-912-609-31	Sequence 31, Appl	
45	35	100.0	9	12			

ALIGNMENTS

RESULT 1
US-09-364-597A-37
; Sequence 37, Application US/09364597A
; Patent No. US20020103130A1
; GENERAL INFORMATION:
; APPLICANT: Ruostantti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: No. US20020103130A1e1 Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Campbell & Flores LLP
; CITY: 4370 La Jolla Village Drive, Suite 700
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,597A
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/159,001
; FILING DATE: 24-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,861
; FILING DATE: 04-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 3419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 535-9001
; TELEFAX: (858) 535-8949

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CC inexpensively synthesised

XX Sequence 5 AA;

Query Match 100.0%; Score 35; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5

Db 1 CRGDC 5

RESULT 14

AD25491
ID ADE25491 standard; peptide; 5 AA.

XX AC ADE25491;

XX DT 29-JAN-2004 (first entry)

XX DE Tc-99m labelled peptide #19.

XX KW Thrombus imaging agent; GPIIb/IIIa receptor; thrombus.

XX OS Synthetic.

XX PN US588474-A.

XX PD 30-MAR-1999.

XX PF 07-JUN-1995; 95US-00478725.

XX PR 08-FEB-1991; 91US-00653012.

XX PR 27-NOV-1991; 91US-00807042.

XX PR 21-MAY-1992; 92US-00886752.

XX PR 22-JUN-1994; 94US-00264176.

XX PR 11-JUL-1994; 94US-00273274.

XX PR 07-JUN-1995; 95US-00480551.

XX PA (DIAT-) DIATIDE INC.

XX PI Dean RT, Lister-James J;

XX DR WPI; 1999-253220/21.

XX PT Reagent for preparing thrombus imaging agent.

XX PS Example 2; Col 12; 17pp; English.

XX The present invention relates to reagents (A) for preparing thrombus imaging agents comprising specific binding peptides (I) and a technetium-99m binding group (II) covalently attached to the specific binding peptide. (I) is a ligand for the GPIIb/IIIa receptor and can be a cyclic or linear peptide not containing the Arg-Gly-Asp (RGD) sequence. (I) are specific for thrombi, and are small and therefore are rapidly cleared from blood and background tissue. (A) are used to produce scintigraphic imaging agents for detection of thrombi in vivo. The present sequence is one such Tc-99m labelled peptide.

XX Sequence 5 AA;

Query Match 100.0%; Score 35; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5

Db 1 CRGDC 5

RESULT 15

AA54976

ID AA54976 standard; peptide; 5 AA.

XX AC AA54976;

XX DT 15-FEB-2000 (first entry)

XX DE Peptide ligand for fibrin polymerisation site.

XX KW Thrombus imaging; fibrin polymerisation site; technetium-99m; Tc-99m; GPIIb/IIIa receptor; cyclic peptide ligand.

XX OS Synthetic.

XX PN US5968476-A.

XX PD 19-OCT-1999.

XX PF 07-JUN-1995; 95US-00484773.

XX PR 21-MAY-1992; 92US-00886052.

XX PR 11-JUL-1994; 94US-00273274.

XX PA (DIAT-) DIATIDE INC.

XX PI Dean RT, Lister-James J;

XX DR WPI; 2000-021733/02.

XX PT A complex used for thrombus imaging comprises technetium-99m complexed with a peptide ligand for GPIIb/IIIa receptor.

XX PS Example 2; Col 13-14; 18pp; English.

XX This sequence represents a peptide ligand for the fibrin polymerisation site. The invention relates to a complex (A) for thrombus imaging comprises technetium-99m (Tc-99m) complexed with a reagent comprising a peptide (P) with 4 to 100 amino acids sequence and a Tc-99m binding moiety covalently bound to (P). (P) is selected from a linear peptide ligand for a GPIIb/IIIa receptor not comprising the amino acid sequence (arginine-glycine-aspartate), a peptide ligand for a polymerisation site of fibrin, and a cyclic peptide ligand for the GPIIb/IIIa receptor. The thrombus imaging reagents provided by the present invention can be used for visualising thrombi in a mammalian body when Tc-99m is labelled

XX Sequence 5 AA;

Query Match 100.0%; Score 35; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5

Db 1 CRGDC 5

Search completed: September 22, 2004, 06:51:44
Job time : 124 secs

PA (DIAT-) DIATIDE INC.
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX Markland FS, Bush LR, Swenson S, Flores Sanchez E;
 PI WPI; 1998-333336/29.
 DR WPI; 1998-333336/29.
 XX New thrombolytic agents - comprise thrombolytic proteinase covalently
 PT linked to targetting compound for binding to component of thrombus.
 PT linked to targetting compound for binding to component of thrombus.
 XX Claim 10; Page 65; 79pp; English.
 PS The invention relates to new thrombolytic agents which comprise a
 XX thrombolytic proteinase covalently linked to a targetting compound
 CC capable of specifically binding to a component of a thrombus. The
 CC thrombolytic agents can be used for eliminating thrombi in vivo in, e.g.
 CC myocardial infarction, cerebral ischaemia, deep vein thrombosis or
 CC pulmonary embolism. A labelled form of the thrombolytic agent can also be
 CC used to image thrombi for diagnostic purposes. The thrombolytic agents
 CC are specifically targetted to thrombus sites in vivo and have minimal
 CC haemorrhagic side effects and side effects related to non-specific
 CC proteolysis. The present sequence represents a specifically claimed
 CC targetting peptide. (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 5 AA;
 SQ Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 DB |||||
 1 CRGDC 5

RESULT 12
 AAW50594
 ID AAW50594 standard; peptide; 5 AA.
 AC AAW50594;
 XX 16-JUL-1998 (first entry)
 DT GPIIb/IIIa receptor ligand with technetium-99m binding moiety.
 DE Technetium-99m label; thrombus imaging; GPIIb/IIIa receptor; ligand;
 XX binding moiety.
 KW Synthetic.
 XX US5736122-A.
 PN 07-APR-1998.
 PD 07-JUN-1995; 95US-00482880.
 PF 08-FEB-1991; 91US-00653012.
 PR 27-NOV-1991; 91US-00807062.
 PR 21-MAY-1992; 92US-00886052.
 PR 22-JUN-1994; 94US-00264176.
 PR 11-JUL-1994; 94US-00273274.
 PR 07-JUN-1995; 95US-00480551.
 XX (DIAT-) DIATIDE INC.
 XX Lister-James J, Dean RT;
 PI WPI; 1998-239148/21.
 DR Reagent useful for preparing thrombus imaging agent - comprises peptide
 PT covalently linked to technetium binding moiety which is technetium
 PT labelled and binds to thrombus component.
 XX

PS Example 2; Col 11-12; 18pp; English.
 XX The invention relates to a reagent for preparing a thrombus imaging
 CC agent. It comprises: (a) a specific binding peptide (BP) having a
 CC sequence of 4-100 amino acids; and (b) a technetium-99m binding moiety
 CC (TBM) covalently linked to the peptide which binds to a component of a
 CC thrombus. TBM forms an electrically neutral complex with technetium-99m.
 CC The small size of the peptide component of the reagent enhances blood and
 CC background tissue clearance and it is easy to prepare. This sequence
 CC represents a GPIIb/IIIa receptor binding peptide covalently linked to a
 CC technetium-99m binding moiety
 XX Sequence 5 AA;
 SQ Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 DB |||||
 1 CRGDC 5

RESULT 13
 AAY21570
 ID AAY21570 standard; peptide; 5 AA.
 AC AAY21570;
 XX 09-AUG-1999 (first entry)
 DT Integrin-binding peptide.
 DE Integrin; fibronectin; vitronectin; extracellular matrix protein;
 KW metastatic; fibronectin adhesion; alphasbeta1 integrin.
 XX Synthetic.
 OS US5912234-A.
 PN 15-JUN-1999.
 PD 03-APR-1996; 96US-00625695.
 PF 27-SEP-1993; 93US-00127422.
 PR 11-MAR-1994; 94US-00212186.
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX Koivunen E, Ruoslahti E;
 PI WPI; 1999-357211/30.
 DR Integrin-binding peptides has specific binding specificity for
 PT fibronectin and vitronectin binding integrins.
 XX Disclosure; Col 15; 16pp; English.
 PS The invention relates to peptides having specific binding specificity for
 CC fibronectin-binding and vitronectin-binding integrins, and in particular
 CC for alphasbeta1 integrin. The peptides can be used in a method of
 CC preventing integrin-mediated attachment to an extracellular matrix
 CC protein, fibronectin, or vitronectin which comprises (a) contacting the
 CC cells with a soluble peptide selected from the sequences shown in
 CC AAY21561, AAY21563 and AAY21586; or (b) contacting the cells with a
 CC soluble peptide comprising the sequence -NGR- selected from the sequences
 CC shown in AAY21564, AAY21566 or AAY21573; or (c) contacting with a soluble
 CC peptide shown in AAY21571. The peptides are useful for inhibiting
 CC metastatic processes with which fibronectin adhesion is associated and also
 CC for inhibiting alpha v beta 1-mediated cell attachment to fibronectin,
 CC and alpha v beta 5-mediated cell attachment to vitronectin. The peptides
 CC are also useful for promoting attachment of integrin expressing cells to
 CC a surface or artificial cell matrix. The peptides can be easily and

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RESULT 9
AAW03492
ID AAW03492 standard; peptide; 5 AA.
XX
XX AC AAW03492;
XX
XX DT 25-MAR-2003 (revised)
XX DT 24-OCT-1996 (first entry)
XX
XX DE Alpha(5)-Beta(1) integrin binding peptide 10.
XX
XX KW Synthetic; fibronectin; vitronectin; integrin; binding motif; adhesion;
XX KW extracellular matrix protein; tumour metastasis.
XX
XX OS Synthetic.
XX
XX PN US5536814-A.
XX
XX PD 16-JUL-1996.
XX
XX PF 11-MAR-1994; 94US-00212186.
XX
XX PR 27-SEP-1993; 93US-00127422.
XX
XX PA (LJOL-) LA JOLLA CANCER RES FOUND.
XX
XX PI Koivunen E, Ruoslahti E;
XX
XX DR WPI; 1996-341556/34.
XX
XX KW Synthetic integrin-binding peptide(s) - useful for inhibiting tumour
XX PT metastasis, etc.
XX
XX PS Disclosure; Col 2; 16pp; English.
XX
XX CC Peptides AAW03483-508 are examples of synthetic peptides generated to
XX CC bind to the fibronectin/vitronectin-binding integrin alpha(5)beta(1).
XX CC They are synthesised to contain the alpha(5)beta(1)-integrin peptide
XX CC binding motifs: DGR, NGR or RGD. The peptides interfere with the binding
XX CC of fibronectin and vitronectin to this integrin and thus may be used to
XX CC block integrin-mediated cell adhesion to extracellular matrix proteins,
XX CC esp. to inhibit tumour metastasis. (Updated on 25-MAR-2003 to correct PF
XX CC field.)
XX
XX SQ Sequence 5 AA;
XX
XX Query Match 100.0%; Score 35; DB 2; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 CRGDC 5
Db |||||
1 CRGDC 5
XX
RESULT 11
AAW64952
ID AAW64952 standard; peptide; 5 AA.
XX
XX AC AAW64952;
XX
XX DT 25-MAR-2003 (revised)
XX DT 23-SEP-1998 (first entry)
XX
XX DE Targetting peptide #45 useful as component of thrombolytic agent.
XX
XX KW Thrombolytic agent; thrombolytic proteinase; blood clot; fibrin;
XX KW thrombus; antithrombotic activity.
XX
XX OS Synthetic.
XX
XX PN WO9824917-A1.
XX
XX PD 11-JUN-1998.
XX
XX PF 02-DEC-1997; 97WO-US021918.
XX
XX PR 02-DEC-1996; 96US-00753781.
XX
XX

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US5721210-A.

24-FEB-1998.

07-JUN-1995; 95US-00485019.

09-JUL-1990; 90US-00550330.

09-JUL-1991; 91WO-US004862.

04-JUN-1993; 93US-00361889.

(TANA) TANABE SEIYAKU CO.

Cardarelli PM, Lobl TJ, Chiang S;

WPI; 1998-168442/15.

New cyclic peptide(s) and peptidomimetic compounds - are integrin receptor antagonists useful in modulating cell adhesion.

Example 9; Col 42; 32pp; English.

The present sequence represents a synthetic peptide which acts as an antagonist to integrin receptors. The invention provides various synthetic peptides which act as cell adhesion modulators because they mimic extra-cellular matrix ligands or other cell adhesion ligands that bind to receptors such as integrin receptors, including fibronectin, laminin, LFA-1, MAC-1, p150,95, vitronectin and gp11b/IIla receptors. Some of the peptides contain the amino acid sequence Arg-Gly-Asp (RGD). Others contain non-RGD sequences, for e.g RCD sequences, and reverse orientation forms of amino acid residues. The synthetic peptides are useful in modulating cell adhesion, including adhesion related to fibronectin, as well as leukocyte adhesion to endothelial cells. They are also claimed to be useful in the study, diagnosis, treatment or prevention of diseases which relate to cell adhesion, e.g. adult respiratory distress syndrome (ARDS), thrombosis and inflammatory conditions

Sequence 5 AA;

Query Match 100.0%; Score 35; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRGDC 5

Db |||||

1 CRGDC 5

RESULT 11

AAW64952

ID AAW64952 standard; peptide; 5 AA.

XX

XX AC AAW64952;

XX

XX DT 25-MAR-2003 (revised)

XX DT 23-SEP-1998 (first entry)

XX

XX DE Targetting peptide #45 useful as component of thrombolytic agent.

XX

XX KW Thrombolytic agent; thrombolytic proteinase; blood clot; fibrin;

XX KW thrombus; antithrombotic activity.

XX

XX OS Synthetic.

XX

XX PN WO9824917-A1.

XX

XX PD 11-JUN-1998.

XX

XX PF 02-DEC-1997; 97WO-US021918.

XX

XX PR 02-DEC-1996; 96US-00753781.

XX

XX WPI; 1992-313678/38.
 XX New synthetic peptide lipids or salts - useful as cell migration
 PT inhibitors, cell adhesion membranes and cell culture bodies.
 XX Disclosure; Page 3; 9pp; Japanese.
 XX The peptide sequence is an example of a highly generic sequence contg.
 CC the RGD motif. Compounds contg. these lipid peptides are useful as cell
 CC migration inhibitors in cell adhesion membranes or cell culture bodies.
 CC See also AAR29048-54
 XX Sequence 5 AA;
 SQ

Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 DB |||||
 1 CRGDC 5

RESULT 7
 AAR69325
 ID AAR69325 standard; peptide; 5 AA.
 XX
 AC AAR69325;
 DT 25-MAR-2003 (revised)
 DT 25-JUN-1995 (first entry)
 XX
 DE Gp IIb/IIIa receptor ligand used in scintigraphic imaging of thrombi.
 KW Scintigraphy; thrombus; thrombi; imaging; specific binding;
 KW technetium-99m; radiolabelled; Gp IIb/IIIa receptor ligand.
 XX Synthetic.
 OS
 XX
 PN WO9323085-A1.
 XX
 PD 25-NOV-1993.
 XX
 PF 21-MAY-1993; 93WO-US004794.
 XX
 PR 21-MAY-1992; 92US-00886752.
 XX
 PA (DIAT-) DIATECH INC.
 PI Dean RT, Lister-James J;
 XX
 DR WPI; 1993-386229/48.
 XX
 PT Reagent for scintigraphic imaging of thrombi with 99m technetium -
 PT comprises synthetic peptide which binds to thrombus covalently coupled to
 PT metal binding gp., rapidly cleared from blood and tissue.
 XX
 PS Claim 41; Page 46; 61pp; English.
 XX
 CC The invention relates to reagents for scintigraphic imaging of a thrombus
 CC in-vivo, comprising (A) a specific binding compound capable of binding to
 CC at least one component of a thrombus, covalently linked to (B) a
 CC technetium-99m-binding moiety. Specific peptides constituting the
 CC reagents are claimed as new. The present peptide is one such peptide.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 5 AA;

Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 DB |||||
 1 CRGDC 5

QY 1 CRGDC 5
 DB |||||
 1 CRGDC 5

RESULT 8
 AAR79093
 ID AAR79093 standard; peptide; 5 AA.
 XX
 AC AAR79093;
 DT 24-JAN-1996 (first entry)
 XX
 DE Alphas/betal integrin binding peptide #20.
 XX
 KW High affinity; integrin binding peptide; alphas/betal; alphas/betas;
 KW alphas/betas3; RGD; stable configuration; wound healing;
 KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;
 KW smooth muscle cell migration.
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..5
 XX
 PN WO9514714-A1.
 XX
 PD 01-JUN-1995.
 XX
 PF 22-NOV-1994; 94WO-US013542.
 XX
 PR 24-NOV-1993; 93US-00158001.
 PR 04-AUG-1994; 94US-00286861.
 XX
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX
 PI Ruoslahti E, Koivunen E;
 DR WPI; 1995-206899/27.
 XX
 PT High affinity integrin binding peptides - can be used to attach cells to
 PT a substrate, inhibit the attachment of osteoclasts to bone, promote wound
 PT healing, inhibit angiogenesis, metastasis of tumours and migration of
 PT smooth muscle cells.
 XX
 PS Example 3; Page 25; 86pp; English.
 XX
 CC The sequences given in AAR76185-200 and AAR79073-94 are high affinity
 CC integrin binding peptides which bind to various integrins. Peptides which
 CC bind to alphas/betal integrins contain the motifs given in AAR76185-86
 CC and peptides which bind to alphas/betas5 and alphas/betas3 integrins
 CC contain the motif given in AAR76187. Alphas/betas5 integrins are also
 CC bound by RGD containing peptides. These peptides assume a
 CC conformationally stabilised configuration which is due to the formation
 CC of a disulphide bond, a peptide bond or a lactam bond. These peptides may
 CC be used for isolating the complementary integrin from a sample mixture by
 CC contacting them under ionic conditions to allow binding of the integrin
 CC to the peptide and then separating the integrin from the peptide. They
 CC can be used for attaching cells to a substrate, by binding them to the
 CC substrate with the cell. The peptides promote wound healing when applied
 CC locally and inhibit the attachment of osteoclasts to bone. They inhibit
 CC angiogenesis, metastasis of tumours and migration of smooth muscle cells
 XX
 SQ Sequence 5 AA;

Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 DB |||||
 1 CRGDC 5

XX 10-APR-1991 (first entry)
 XX Fibrinogen receptor antagonising peptide (VI).
 DE Fibrinogen receptor antagonist; platelet aggregation; thrombosis;
 XX myocardial infarction.
 KW Synthetic.
 XX Key Location/Qualifiers
 FT Disulfide-bond 1. 5
 FT Modified-site 1. 1
 FT /label= homoCys
 XX EP410537-A.
 XX 30-JAN-1991.
 XX 23-JUL-1990; 90EP-00202015.
 XX 28-JUL-1989; 89US-00386534.
 XX (MERI) MERCK & CO INC.
 XX Nutt RF, Brady SF, Veber DF;
 XX WPI; 1991-030928/05.
 XX New fibrinogen receptor antagonising peptide cpds. - used to inhibit
 PT blood platelet aggregation during surgery on peripheral arteries and in
 PT cardiovascular surgery.
 XX Claim 7; Page 10; 10pp; English.
 XX To residue homoCys1 is attached Acetyl and to residue Cys5 is attached
 CC NH2. The peptide is prep. using standard methods of solid phase
 CC synthesis and is one of 17 pref. examples of a highly generic formula.
 CC The peptide is used to inhibit fibrinogen-induced platelet aggregation
 CC and is partic. useful because it does not significantly deplete the
 CC platelet count. It has a relatively short duration of activity and is
 CC thus useful where prevention of platelet aggregation over a short period
 CC of time is desirable, e.g. in surgery of peripheral arteries and
 CC cardiovascular surgery. It is also useful in prevention of platelet
 CC thrombosis, thromboembolism and reocclusion either during and after
 CC thrombolytic therapy, or after angioplasty of coronary and other arteries
 CC and after coronary artery by-pass procedures, or to prevent myocardial
 CC infarction. It may be combined with thrombolytic agents, e.g. plasminogen
 CC activators or streptokinase, or anticoagulants. See also AAR10413-18 and
 CC EP-410537, EP-410539, EP-410540, EP-410541, and EP-410767
 XX Sequence 5 AA;
 SQ
 Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 DB 1 CRGDC 5
 RESULT 5
 AAR27031
 ID AAR27031 standard; peptide; 5 AA.
 XX AAR27031;
 AC AAR27031;
 XX 20-MAY-1998 (first entry)
 DT Peptide lipid contg. RGD.
 DE Synthetic; cell migration; inhibitor; cell adhesion membrane;
 KW (FUJIF) FUJI PHOTO FILM CO LTD.

KW cell culture body.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH modified_site 1
 FT /note= "acylated"
 FT modified_site 5
 FT /note= "alkylated"
 XX JP04221395-A.
 PN 11-AUG-1992.
 XX 29-NOV-1990; 90JP-00333336.
 XX 26-OCT-1990; 90JP-00289494.
 XX (FUJIF) FUJI PHOTO FILM CO LTD.
 XX WPI; 1992-313679/38.
 XX New synthetic peptide lipid(s) and salts - useful as cell migration
 PT inhibitors, cell adhesion membranes or cell culture bodies.
 XX Disclosure; Page 3; 9pp; Japanese.
 XX The peptide sequence is an example of a highly generic sequence contg.
 CC the RGD motif. Compounds contg. these lipid peptides are useful as cell
 CC migration inhibitors in cell adhesion membranes or cell culture bodies.
 CC See also AAR27027-33
 XX Sequence 5 AA;
 SQ
 Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 DB 1 CRGDC 5
 RESULT 6
 AAR29052
 ID AAR29052 standard; peptide; 5 AA.
 XX AAR29052;
 AC AAR29052;
 XX 20-MAY-1998 (first entry)
 DT Peptide lipid contg. RGD.
 DE Synthetic.
 XX Synthetic; cell migration; inhibitor; cell adhesion membrane;
 KW cell culture body.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH modified_site 1
 FT /note= "acylated"
 FT modified_site 5
 FT /note= "alkylated"
 XX JP04221394-A.
 PN 11-AUG-1992.
 XX 29-NOV-1990; 90JP-00333335.
 XX 26-OCT-1990; 90JP-00289493.
 XX (FUJIF) FUJI PHOTO FILM CO LTD.

Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 DB 1 CRGDC 5

RESULT 2
 AAR10415
 ID AAR10415 standard; protein; 5 AA.
 XX AAR10415;
 AC AAR10415;
 DT 10-APR-1991 (first entry)
 DE Fibrinogen receptor antagonising peptide (III).
 XX Fibrinogen receptor antagonist; platelet aggregation; thrombosis;
 KW myocardial infarction.
 XX Synthetic.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..5
 FT Modified-site 1..1
 FT /label= N-MethylCys
 XX EP410537-A.
 PN 30-JAN-1991.
 XX 23-JUL-1990; 90EP-00202015.
 PF 28-JUL-1989; 89US-00386534.
 PR (MERI) MERCK & CO INC.
 PA Nutt RF, Brady SF, Veber DF;
 XX WPI; 1991-030928/05.
 DR New fibrinogen receptor antagonising peptide cpds. - used to inhibit
 XX blood platelet aggregation during surgery on peripheral arteries and in
 XX cardiovascular surgery.
 XX Claim 5; Page 10; 10pp; English.

To residue N-MethylCys1 is attached Acetyl and to residue Cys5 is attached OH. The peptide is prepd. using standard methods of solid phase synthesis and is one of 17 pref. examples of a highly generic formula. The peptide is used to inhibit fibrinogen-induced platelet aggregation and is partic. useful because it does not significantly deplete the platelet count. It has a relatively short duration of activity and is thus useful in prevention of platelet aggregation over a short period of time is desirable, e.g. in surgery of peripheral arteries and cardiovascular surgery. It is also useful in prevention of platelet thrombosis, thromboembolism and reocclusion either during and after thrombolytic therapy, or after angioplasty of coronary and other arteries and after coronary artery by-pass procedures, or to prevent myocardial infarction. It may be combined with thrombolytic agents, e.g. plasminogen activators or streptokinase, or anticoagulants. See also AAR10413-18 and EP-410541, and EP-410767

Sequence 5 AA;
 Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 DB 1 CRGDC 5

RESULT 3
 AAR10414
 ID AAR10414 standard; protein; 5 AA.
 XX AAR10414;
 AC AAR10414;
 DT 10-APR-1991 (first entry)
 DE Fibrinogen receptor antagonising peptide (III).
 XX Fibrinogen receptor antagonist; platelet aggregation; thrombosis;
 KW myocardial infarction.
 XX Synthetic.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..5
 FT Modified-site 1..1
 FT /label= N-MethylCys
 XX EP410537-A.
 PN 30-JAN-1991.
 XX 23-JUL-1990; 90EP-00202015.
 PF 28-JUL-1989; 89US-00386534.
 PR (MERI) MERCK & CO INC.
 PA Nutt RF, Brady SF, Veber DF;
 XX WPI; 1991-030928/05.
 DR New fibrinogen receptor antagonising peptide cpds. - used to inhibit
 XX blood platelet aggregation during surgery on peripheral arteries and in
 XX cardiovascular surgery.
 XX Claim 4; Page 10; 10pp; English.

To residue Cys5 is attached OH. The peptide is prepd. using standard methods of solid phase synthesis and is one of 17 pref. examples of a highly generic formula. The peptide is used to inhibit fibrinogen-induced platelet aggregation and is partic. useful because it does not significantly deplete the platelet count. It has a relatively short duration of activity and is thus useful in prevention of platelet aggregation over a short period of time is desirable, e.g. in surgery of peripheral arteries and cardiovascular surgery. It is also useful in prevention of platelet thrombosis, thromboembolism and reocclusion either during and after thrombolytic therapy, or after angioplasty of coronary and other arteries and after coronary artery by-pass procedures, or to prevent myocardial infarction. It may be combined with thrombolytic agents, e.g. plasminogen activators or streptokinase, or anticoagulants. See also AAR10413-18 and EP-410537, EP-410539, EP-410540, EP-410541, and EP-410767

Sequence 5 AA;
 Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 DB 1 CRGDC 5

RESULT 4
 AAR10418
 ID AAR10418 standard; protein; 5 AA.
 XX AAR10418;
 AC AAR10418;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2004, 06:38:56 ; Search time 121 Seconds
(without alignments)
11.676 Million cell updates/sec

Title: US-09-912-609-9

Perfect score: 35

Sequence: 1 CRGDC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	5	2 AAR11587	Aar11587 Fibrinoge
2	35	100.0	5	2 AAR10415	Aar10415 Fibrinoge
3	35	100.0	5	2 AAR10414	Aar10414 Fibrinoge
4	35	100.0	5	2 AAR10418	Aar10418 Fibrinoge
5	35	100.0	5	2 AAR27031	Aar27031 Peptide 1
6	35	100.0	5	2 AAR29052	Aar29052 Peptide 1
7	35	100.0	5	2 AAR69325	Aar69325 Gp Iib/Ii
8	35	100.0	5	2 AAR79093	Aar79093 Alphas/be
9	35	100.0	5	2 AAW03492	Aaw03492 Alpha(5)-
10	35	100.0	5	2 AAW48499	Aaw48499 Integrin
11	35	100.0	5	2 AAW64952	Aaw64952 Targettin
12	35	100.0	5	2 AAW50594	Aaw50594 GPIIb/III
13	35	100.0	5	2 AAY21570	Aay21570 Integrin-
14	35	100.0	5	2 ADE25491	Ade25491 Tc-99m la
15	35	100.0	5	3 AAY54976	Aay54976 Peptide 1
16	35	100.0	5	3 AAY95465	Aay95465 GPIIb/III
17	35	100.0	5	3 AAE17982	Aae17982 Human lig
18	35	100.0	5	6 ABUS9650	Abus9650 Fibrinonec
19	35	100.0	6	2 AAR76191	Aar76191 Alphav/be
20	35	100.0	6	2 AAW03508	Aaw03508 Alpha(5)-
21	35	100.0	6	2 AAW03483	Aaw03483 Alpha(5)-
22	35	100.0	6	2 AAW35454	Aaw35454 Non-dendr
23	35	100.0	6	2 AAW35453	Aaw35453 Non-dendr
24	35	100.0	6	2 AAY21561	Aay21561 Integrin-
25	35	100.0	6	2 AAY21586	Aay21586 Integrin-

26	35	100.0	6	5 AAM48797	Aam48797 Tumour-ta
27	35	100.0	6	6 ABUS9535	Abus9535 Fibrinonec
28	35	100.0	6	6 ABUS9538	Abus9538 Fibrinonec
29	35	100.0	7	2 AAY43232	Aay43232 RGD-conta
30	35	100.0	7	3 AAY90212	Aay90212 Alphav in
31	35	100.0	7	3 AAY90219	Aay90219 UPAR targ
32	35	100.0	8	6 ABP98675	Abp98675 Cyclic RG
33	35	100.0	9	2 AAR79074	Aar79074 Alphav/be
34	35	100.0	9	2 AAR76200	Aar76200 Alphav/be
35	35	100.0	9	2 AAR79073	Aar79073 Alphav/be
36	35	100.0	9	2 AAR76199	Aar76199 Alphav/be
37	35	100.0	9	2 AAR79089	Aar79089 Alphav/be
38	35	100.0	9	2 AAW01131	Aaw01131 RGD pepti
39	35	100.0	9	2 AAW60289	Aaw60289 Tumour ho
40	35	100.0	9	2 AAW56034	Aaw56034 Chimeric
41	35	100.0	9	2 AAW56035	Aaw56035 Chimeric
42	35	100.0	9	2 AAY42255	Aay42255 Synthetic
43	35	100.0	9	2 AAY43233	Aay43233 RGD-conta
44	35	100.0	9	2 AAW93626	Aaw93626 NGR recep
45	35	100.0	9	2 AAY48821	Aay48821 Membrane

ALIGNMENTS

RESULT 1
AAR11587
ID AAR11587 standard; protein; 5 AA.
XX AAR11587;
AC AAR11587;
XX 12-JUN-1991 (first entry)
DT Fibrinogen receptor antagonist #4.
DE fibrinogen receptor antagonist;
KW fibrinogen receptor antagonist; thrombosis; fibrinogen;
KW Iib/Iiia receptor.
XX Synthetic.
OS Key Location/Qualifiers
FH Disulfide-bond 1. .5
FT Modified-site 2 /label= Arg(phenyl)
FT EP422938-A.
XX 17-APR-1991.
PD 11-OCT-1990; 90EP-00311151.
XX 13-OCT-1989; 89US-00421224.
XX (MERI) MERCK & CO INC.
XX Nutt RF, Brady ST, Veber KF, Duggan MF;
XX WPI; 1991-111423/16.
XX Polypeptide fibrinogen receptor antagonists - used to prevent thrombosis,
XX e.g. during cardiovascular surgery.
XX Disclosure; Page 7; 16pp; English.
XX Cys at position 1 carries an acetyl group. The peptide inhibits binding
XX of fibrinogen to the platelet membrane glycoprotein complex Iib/Iiia
XX receptor. It may be used to prevent post-operative thrombosis,
XX thromboembolism and reocclusion, platelet adhesion in extracorporeal
XX blood circulation systems and to prevent myocardial infarction. See also
XX AAR11584-6 and AAR11588-R11594
XX Sequence 5 AA;

Query Match 100.0%; Score 35; DB 16; Length 477;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5

Db 444 CRGDC 448

Search completed: September 22, 2004, 06:54:58
Job time : 117 secs

GN ATPD.
OS Tropheryma whippelii (Whipple's bacillus) (Tropheryma whippelii).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Cellulomonadaceae; Tropheryma.
ON NCBI_TaxID=2039;
OX [1]
RP SEQUENCE FROM N.A.
RA Matwald M., Lepp P.W., Relman D.A.;
RT "Analysis of conserved non-rRNA genes of Tropheryma whippelii:
RT implications for genome structure, strain typing, and phylogenetic
RT relationships.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF483648; AAO84483.1; -;
DR GO; GO:0045225; C:hydrogen-translocating F-type ATPase complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005224; F:ATP-binding and phosphorylation-dependent c. . .; IEA.
DR GO; GO:0008553; F:hydrogen-exporting ATPase activity, phospho. . .; IEA.
DR GO; GO:0046933; F:hydrogen-translocating ATP synthase activity. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR InterPro; IPR004100; ATPase_a/bN.
DR InterPro; IPR00793; ATPase_a/b C.
DR InterPro; IPR005722; ATP synthFI beta.
DR InterPro; IPR009005; F1 ATPase_a/bN.
DR Pfam; PF00006; ATP-synt_ab; 1.
DR Pfam; PF00306; ATP-synt_ab_C; 1.
DR Pfam; PF02874; ATP-synt_ab_N; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR01039; atpD; 1.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
DR KW Hydrolyase; Complete proteome.
DR SQ SEQUENCE 474 AA; 52086 MW; 2D4AD8828A37F48C CRC64;
Query Match 100.0%; Score 35; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CRGDC 5
DB 441 CRGDC 445

RESULT 14
Q83HYO PRELIMINARY; PRT; 474 AA.
ID Q83HYO
AC Q83HYO; (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE ATP synthase beta chain (EC 3.6.3.14).
GN ATPD OR TW344.
OS Tropheryma whippelii (strain TW08/27) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=218496;
ON [1]
RP SEQUENCE FROM N.A.
RA Bentley S.D., Matwald M., Murphy L.D., Pallen M.J., Yeats C.A.,
RA Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.E.,
RA von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
RA Barrell B.G., Parkhill J., Relman D.A.;
RT "Sequencing and analysis of the genome of the Whipple's disease
RT bacterium Tropheryma whippelii.";
RL Lancet 361:637-644 (2003).
DR EMBL; BX251411; CAD67016.1; -;
DR GO; GO:0045225; C:hydrogen-translocating F-type ATPase complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005224; F:ATP-binding and phosphorylation-dependent c. . .; IEA.
DR GO; GO:0008553; F:hydrogen-exporting ATPase activity, phospho. . .; IEA.
DR GO; GO:0046933; F:hydrogen-translocating ATP synthase activity. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR InterPro; IPR004100; ATPase_a/bN.
DR InterPro; IPR00793; ATPase_a/b C.
DR InterPro; IPR005722; ATP synthFI beta.
DR InterPro; IPR009005; F1 ATPase_a/bN.
DR Pfam; PF00006; ATP-synt_ab; 1.
DR Pfam; PF00306; ATP-synt_ab_C; 1.
DR Pfam; PF02874; ATP-synt_ab_N; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR01039; atpD; 1.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
DR KW Hydrolyase; Complete proteome.
DR SQ SEQUENCE 474 AA; 52086 MW; 2D4AD8828A37F48C CRC64;
Query Match 100.0%; Score 35; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CRGDC 5
DB 441 CRGDC 445

DR GO; GO:0003936; F:hydrogen-translocating two-sector ATPase act. . .; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0001666; F:nucleotide binding; IEA.
DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR InterPro; IPR004100; ATPase_a/bN.
DR InterPro; IPR00793; ATPase_a/b C.
DR InterPro; IPR005722; ATP synthFI beta.
DR InterPro; IPR009005; F1 ATPase_a/bN.
DR Pfam; PF00006; ATP-synt_ab; 1.
DR Pfam; PF00306; ATP-synt_ab_C; 1.
DR Pfam; PF02874; ATP-synt_ab_N; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR01039; atpD; 1.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
DR KW Hydrolyase; Complete proteome.
DR SQ SEQUENCE 474 AA; 52086 MW; 2D4AD8828A37F48C CRC64;
Query Match 100.0%; Score 35; DB 16; Length 474;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CRGDC 5
DB 441 CRGDC 445

RESULT 15
Q83G91 PRELIMINARY; PRT; 477 AA.
ID Q83G91
AC Q83G91; (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE ATP synthase beta chain (EC 3.6.1.34).
GN ATPD OR TW424.
OS Tropheryma whippelii (strain Twist) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=203267;
ON [1]
RP SEQUENCE FROM N.A.
RA Raoult D., Audic S., Robert C., Ogata H., Suhre K., Drancourt M.,
RA Claverie J.-M.;
RT "Tropheryma whippelii illustrates the diversity of gene loss patterns
RT in small genome bacterial pathogens.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016851; AAO44521.1; -;
DR GO; GO:0045225; C:hydrogen-translocating F-type ATPase complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005224; F:ATP-binding and phosphorylation-dependent c. . .; IEA.
DR GO; GO:0008553; F:hydrogen-exporting ATPase activity, phospho. . .; IEA.
DR GO; GO:0046933; F:hydrogen-translocating ATP synthase activity. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR InterPro; IPR004100; ATPase_a/bN.
DR InterPro; IPR00793; ATPase_a/b C.
DR InterPro; IPR005722; ATP synthFI beta.
DR InterPro; IPR009005; F1 ATPase_a/bN.
DR Pfam; PF00006; ATP-synt_ab; 1.
DR Pfam; PF00306; ATP-synt_ab_C; 1.
DR Pfam; PF02874; ATP-synt_ab_N; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR01039; atpD; 1.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
DR KW Hydrolyase; Complete proteome.
DR SQ SEQUENCE 477 AA; 52459 MW; 000E1063A50782DE CRC64;

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KW Hypothetical protein.
SQ SEQUENCE 336 AA; 37667 MW; FD51D95493576F71 CRC64;
  Query Match 100.0%; Score 35; DB 12; Length 279;
  Best Local Similarity 100.0%; Pred. No. 26;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 254 CRGDC 258

RESULT 10
Q8VA50 PRELIMINARY; PRT; 335 AA.
AC Q8VA50;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glycoprotein (Fragment).
GN E1.
OS Ag80-663 virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=166978;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21465035; PubMed=11581380;
RA Powers A.M., Brault A.C., Shirako Y., Strauss E.G., Kang W.,
RA Strauss J.H., Weaver S.C.;
RT "Evolutionary relationships and systematics of the alphaviruses.";
RL J. Virol. 75:10118-10131(2001).
DR EMBL; AF398388; AAL35787.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002548; Alpha_E1_glycop.
DR InterPro; IPR000336; Flavi_glycoprote.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF01589; Alpha_E1_glycop; 1.
FT NON_TER 1
FT NON_TER 335
SQ SEQUENCE 335 AA; 36014 MW; A584EAC07D3948AE CRC64;

  Query Match 100.0%; Score 35; DB 12; Length 335;
  Best Local Similarity 100.0%; Pred. No. 30;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 286 CRGDC 290

RESULT 11
Q8NCQ7 PRELIMINARY; PRT; 336 AA.
AC Q8NCQ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Scrausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029574; AAH29574.1; -.
DR GO; GO:0003509; F:calcium ion binding; IEA.
DR GO; GO:004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR PROSITE; PS00118; PA2_HIS; 1.

KW Hypothetical protein.
SQ SEQUENCE 336 AA; 37667 MW; FD51D95493576F71 CRC64;
  Query Match 100.0%; Score 35; DB 4; Length 336;
  Best Local Similarity 100.0%; Pred. No. 30;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 29 CRGDC 33

RESULT 12
Q9CW26 PRELIMINARY; PRT; 353 AA.
AC Q9CW26;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 150001601ORik protein (Fragment).
GN 150001601ORIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gusninch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK005271; BAB23923.1; -.
DR MGD; MGI:1916202; 150001601ORik.
DR InterPro; IPR006634; TLC.
DR SMART; SM00724; TLC; 1.
FT NON_TER 1
FT NON_TER 353
SQ SEQUENCE 353 AA; 38897 MW; E989E015AEC83C0A CRC64;

  Query Match 100.0%; Score 35; DB 11; Length 353;
  Best Local Similarity 100.0%; Pred. No. 31;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 284 CRGDC 288

RESULT 13
Q84DX6 PRELIMINARY; PRT; 474 AA.
AC Q84DX6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ATP synthase F1 complex beta chain.

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RA Moravec T., Cerowska N., Pecenkova T., Nielsen S.L., Vlcek C.;
RL "The nucleotide sequence of potato mop-top isolate 54-15."
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY187010; AAC32789.1; -.
DR InterPro; IPR001896; Plant_vir_prot.
DR Pfam; PF01307; Plant_vir_prot; 1.
SQ SEQUENCE 119 AA; 13154 MW; D2D37B6768305932 CRC64;

Query Match 100.0%; Score 35; DB 12; Length 119;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 109 CRGDC 113

RESULT 7
Q8BMZ3 PRELIMINARY; PRT; 189 AA.
AC Q8BMZ3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tafazzin homolog.
GN TAZ OR 9130012G04RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=BODY;
RX MEDLINE=223154683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK004035; BAC25063.1; -.
DR MGD; MGI:109626; Taz.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002123; Acyltransferase.
DR InterPro; IPR000872; Tafazzin.
DR Pfam; PF01553; Acyltransferase; 1.
DR PRINTS; PR00979; TAFAZZIN.
DR SMART; SM00563; Flsc; 1.
SQ SEQUENCE 189 AA; 21863 MW; 123BCACA40B78BFC CRC64;

Query Match 100.0%; Score 35; DB 11; Length 189;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 122 CRGDC 126

RESULT 8
Q851N3 PRELIMINARY; PRT; 218 AA.
AC Q851N3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OSJNBA0042109.11.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;

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RN SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNBA0042109 genomic sequence."
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC104487; AAC41141.1; -.
KW Hypothetical protein.
SQ SEQUENCE 218 AA; 24562 MW; 4FE0A501AA17507 CRC64;

Query Match 100.0%; Score 35; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 203 CRGDC 207

RESULT 9
Q8JL35 PRELIMINARY; PRT; 279 AA.
AC Q8JL35;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Virus phiCh1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=114777;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20177831; PubMed=10712697;
RX Baranyi U., Klein R., Lubitz W., Kruger D.H., Witte A.;
RT "The archaeal haloalkaliphilic virus-encoded Dam-like methyltransferase M.
RT phiCh1-I methylates adenine residues and complements dam mutants in
RT the low salt environment of Escherichia coli."
RL Mol. Microbiol. 35:1168-1179(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20497008; PubMed=11040128;
RA Klein R., Greineder B., Baranyi U., Witte A.;
RT "The structural protein E of the archaeal virus phiCh1: evidence for
RT processing in Natrialba magadii during virus maturation."
RL Virology 276:376-387(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22136043; PubMed=12139629;
RA Klein R., Baranyi U., Rossler N., Greineder B., Scholz H., Witte A.;
RT "Natrialba magadii virus phiCh1: first complete nucleotide sequence
RT and functional organization of a virus infecting a haloalkaliphilic
RT archaeon."
RL Mol. Microbiol. 45:851-863(2002).
RN [4]
RP SEQUENCE FROM N.A.
RA Klein R., Baranyi U., Rossler N., Greineder B., Scholz H.;
RT "Sequence analysis of the temperate virus phiCh1 infecting the
RT haloalkaliphilic archaeon Natrialba magadii."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440695; AM98695.1; -.
DR InterPro; IPR003615; HNH_nuc.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 1.
DR SMART; SM00507; HNH; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PSS0157; ZINC_FINGER_C2H2_2; 1.
DR Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 279 AA; 31698 MW; 2A47BFE882306E13 CRC64;

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O92517
 ID O92517 PRELIMINARY; PRT; 118 AA.
 AC O92517;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Second triple gene block gene.
 OS Beet virus Q.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 OX NCBI_TaxID=71972;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98378056; PubMed=9714254;
 RA Koenig R., Pleij C., Beter C., Commandeur U.;
 RT "Genome properties of beet virus Q, a new furo-like virus from
 RT sugarbeet, determined from unpurified virus.";
 RL J. Gen. Virol. 79:2027-2036 (1998).
 DR EMBL; AJ223598; CAA11463.1; -
 DR InterPro; IPR001896; Plant_vir_prot.
 DR Pfam; PF01307; Plant_vir_prot; 1.
 DR ProDom; PD001561; Plant_vir_prot; 1.
 SQ SEQUENCE 118 AA; 12719 MW; A55EF6BC198123EB CRC64;
 Query Match 100.0%; Score 35; DB 12; Length 118;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 Db 109 CRGDC 113
 RESULT 3
 Q9YPH2 PRELIMINARY; PRT; 118 AA.
 ID Q9YPH2
 AC Q9YPH2;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Triple-gene-block second protein.
 OS Broad bean necrosis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 OX NCBI_TaxID=79918;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98390102; PubMed=9722878;
 RA Lu X., Yamamoto S., Tanaka M., Hibi T., Namba S.;
 RT "The genome organization of the broad bean necrosis virus (BBNV).";
 RL Arch. Virol. 143:1335-1348 (1998).
 DR EMBL; D86638; BAA34697.1; -
 DR InterPro; IPR001896; Plant_vir_prot.
 DR Pfam; PF01307; Plant_vir_prot; 1.
 DR ProDom; PD001561; Plant_vir_prot; 1.
 SQ SEQUENCE 118 AA; 13255 MW; F7EC57D303FDS5A CRC64;
 Query Match 100.0%; Score 35; DB 12; Length 118;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 Db 110 CRGDC 114
 RESULT 4
 Q9IV53 PRELIMINARY; PRT; 119 AA.
 ID Q9IV53
 AC Q9IV53;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Triple-gene-block protein 2.
 GN TGBP2.

OS Potato mop-top virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 OX NCBI_TaxID=37128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swedish;
 RA Savenkov E.I., Sandgren M., Germundsson A.;
 RT "Complete sequence of RNA2 from Potato mop-top virus (PMTV-Sw).";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ277556; CAB91102.1; -
 DR InterPro; IPR001896; Plant_vir_prot.
 DR Pfam; PF01307; Plant_vir_prot; 1.
 DR ProDom; PD001561; Plant_vir_prot; 1.
 SQ SEQUENCE 119 AA; 13123 MW; CFI5C8BC03305932 CRC64;
 Query Match 100.0%; Score 35; DB 12; Length 119;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 Db 109 CRGDC 113
 RESULT 5
 Q85292 PRELIMINARY; PRT; 119 AA.
 ID Q85292
 AC Q85292;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 13K protein.
 OS Potato mop-top virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 OX NCBI_TaxID=37128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Toad;
 RX MEDLINE=95088602; PubMed=7996148;
 RA Scott K.P., Kashiwazaki S., Reavy B., Harrison B.D.;
 RT "The nucleotide sequence and potato mop-top virus RNA 2: a novel type
 RT of genome organization for a furovirus.";
 RL J. Gen. Virol. 75:3561-3568 (1994).
 DR EMBL; D30753; BAA06413.1; -
 DR InterPro; IPR001896; Plant_vir_prot.
 DR Pfam; PF01307; Plant_vir_prot; 1.
 DR ProDom; PD001561; Plant_vir_prot; 1.
 SQ SEQUENCE 119 AA; 13109 MW; CFI36F869821B8C2 CRC64;
 Query Match 100.0%; Score 35; DB 12; Length 119;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 Db 109 CRGDC 113
 RESULT 6
 Q80QA2 PRELIMINARY; PRT; 119 AA.
 ID Q80QA2
 AC Q80QA2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Triple gene block protein 13K.
 GN TGBP2.
 OS Potato mop-top virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 OX NCBI_TaxID=37128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=54-15;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2004, 06:47:32 ; Search time 115 Seconds
(without alignments)
13.718 Million cell updates/sec

Title: US-09-912-609-9
Perfect score: 35
Sequence: 1 CRGDC 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25.*

- 1: sp_arches.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_ricent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_ivirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	88	12 Q88801	Q88801 eastern equ
2	35	100.0	118	12 Q92517	Q92517 beet virus
3	35	100.0	118	12 Q9YF2	Q9YF2 broad bean
4	35	100.0	119	12 Q9IV53	Q9IV53 potato mop-
5	35	100.0	119	12 Q85292	Q85292 potato mop-
6	35	100.0	119	12 Q80QA2	Q80QA2 potato mop-
7	35	100.0	189	11 Q8BM23	Q8BM23 mus musculus
8	35	100.0	218	10 Q85LN3	Q85LN3 oryza sativ
9	35	100.0	279	12 Q8JL35	Q8JL35 virus phich
10	35	100.0	335	12 Q8VA50	Q8VA50 ag80-663 vi
11	35	100.0	336	4 Q8NCQ7	Q8NCQ7 homo sapien
12	35	100.0	353	11 Q9CW26	Q9CW26 mus musculu
13	35	100.0	474	2 Q84DX6	Q84DX6 tropheryma
14	35	100.0	474	16 Q83HY0	Q83HY0 tropheryma
15	35	100.0	477	16 Q83G91	Q83G91 tropheryma
16	35	100.0	546	12 Q80IB8	Q80IB8 influenza a

17	35	100.0	549	12 Q80IA8	Q80IA8 influenza a
18	35	100.0	552	12 Q80IC9	Q80IC9 influenza a
19	35	100.0	552	12 Q80IC5	Q80IC5 influenza a
20	35	100.0	552	12 Q80IB9	Q80IB9 influenza a
21	35	100.0	552	12 Q80IB7	Q80IB7 influenza a
22	35	100.0	552	12 Q80IA1	Q80IA1 influenza a
23	35	100.0	552	12 Q80I97	Q80I97 influenza a
24	35	100.0	552	12 Q80I95	Q80I95 influenza a
25	35	100.0	552	12 Q80I82	Q80I82 influenza a
26	35	100.0	567	12 Q9E7Q7	Q9E7Q7 influenza a
27	35	100.0	691	13 Q7T193	Q7T193 pagrus majo
28	35	100.0	954	5 Q9YGC8	Q9YGC8 caenorhabdi
29	35	100.0	1253	12 Q9YKC6	Q9YKC6 venezuelan
30	35	100.0	1258	12 Q9WC27	Q9WC27 venezuelan
31	32	91.4	28	13 Q8AYF9	Q8AYF9 salmo trutt
32	32	91.4	88	12 Q8815	Q8815 eastern equ
33	32	91.4	88	12 Q8810	Q8810 eastern equ
34	32	91.4	88	12 Q8803	Q8803 eastern equ
35	32	91.4	88	12 Q8816	Q8816 eastern equ
36	32	91.4	88	12 Q8811	Q8811 eastern equ
37	32	91.4	88	12 Q8817	Q8817 eastern equ
38	32	91.4	88	12 Q8809	Q8809 eastern equ
39	32	91.4	88	12 Q8823	Q8823 eastern equ
40	32	91.4	88	12 Q8808	Q8808 eastern equ
41	32	91.4	88	12 Q8818	Q8818 eastern equ
42	32	91.4	88	12 Q8821	Q8821 eastern equ
43	32	91.4	88	12 Q8807	Q8807 eastern equ
44	32	91.4	88	12 Q8804	Q8804 eastern equ
45	32	91.4	88	12 Q8822	Q8822 eastern equ

ALIGNMENTS

RESULT 1

Q88801 ID Q88801 PRELIMINARY; PRT; 88 AA.
AC Q88801;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E1 protein (Fragment).
OS Eastern equine encephalitis virus (Eastern equine encephalomyelitis virus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphaviruses.
OC Alphavirus.
OX NCBI_TaxID=11021;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10365;
RX MEDLINE=94076404; PubMed=8254725;
RA Weaver S.C., Hagenbaugh A., Bellow L.A., Gousset L., Mallampalli V., Holland J.J., Scott T.W.;
RT "Evolution of alphaviruses in the eastern equine encephalomyelitis complex.";
RL J. Virol. 68:158-169(1994).
DR EMBL; U01577; AAC53764.1; -;
DR InterPro; IPR002548; Alpha_E1_glycop.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF01589; Alpha_E1_glycop; 1.
FT NON TER 1
SQ SEQUENCE 88 AA; 9540 MW; CBB34D04C62C196F CRC64;

Query Match 100.0%; Score 35; DB 12; Length 88;

Best Local Similarity 100.0%; Pred. No. 9.6;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5

Db 24 CRGDC 28

RESULT 2

FT CHAIN 757 812 6 kDa PEPTIDE.
 FT CHAIN 813 1254 SPIKE GLYCOPROTEIN E1.
 FT ACT_SITE 151 151 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 157 157 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 225 225 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT TRANSMEM 701 721 POTENTIAL.
 FT TRANSMEM 794 813 POTENTIAL.
 FT TRANSMEM 1231 1248 POTENTIAL.
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 545 545 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 651 651 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 946 946 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1254 AA; 138337 MW; 29DDBF37F9E92C4B CRC64;

Query Match 91.4%; Score 32; DB 1; Length 1254;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRGDC 5
 Db 1188 CKGDC 1192

RESULT 15

POLS BEVVM STANDARD; PRT; 1254 AA.
 AC P36331; Q66587; Q66588; Q66589; Q66590; Q66591;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Structural polyprotein (P130) [Contains: Coat protein C (SC 3.4.21.-)
 DE (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
 DE 6 kDa peptide; Spike glycoprotein E1].
 OS Venezuelan equine encephalitis virus (strain Mena II).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 OC Alphavirus.
 OC NCBI_TaxID=36384;
 RN [1]

SEQUENCE FROM N.A.
 RX MEDLINE=93187617; PubMed=8445371;
 RA Snider J.M., Kinney R.M., Tsuchiya K.R., Trent D.W.;
 RT "Molecular evidence that epizootic Venezuelan equine encephalitis
 RT (VEE) I-AB viruses are not evolutionary derivatives of enzootic VEE
 RT subtype I-E or II viruses."
 RL J. Gen. Virol. 74:519-523(1993).
 CC -!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
 CC -!- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
 CC -!- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL
 CC SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
 CC HEMAGGLUTININ.
 CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
 CC -----
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 CC -----

DR EMBL; L04599; AAA42990.1; -
 DR EMBL; L04599; AAA42989.1; ALT TERM.
 DR EMBL; L04599; AAA42991.1; ALT SEQ.
 DR EMBL; L04599; AAA42992.1; ALT SEQ.
 DR EMBL; L04599; AAA42993.1; ALT SEQ.
 DR EMBL; L04599; AAA42994.1; ALT INIT.
 DR PIR; JQ1979; JQ1979.
 DR HSSP; P03315; 1VCP.
 DR MEROPS; S03.001; -
 DR InterPro; IPR002548; Alpha_E1_glycop.
 DR InterPro; IPR000936; Alpha_E2_glycop.
 DR InterPro; IPR002533; Alpha_E3_glycop.

DR InterPro; IPR009003; Cys_Ser trypsin.
 DR InterPro; IPR000336; Flavi_glycoprote.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000930; Peptidase_S3.
 DR Pfam; PF00944; Alpha_core; 1.
 DR Pfam; PF01589; Alpha_E1_glycop; 1.
 DR Pfam; PF00943; Alpha_E2_glycop; 1.
 DR Pfam; PF01563; Alpha_E3_glycop; 1.
 DR PRINTS; PR00798; TOGAVIRIN.
 KW Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
 KW Serine protease.
 FT CHAIN 1 274 COAT PROTEIN C.
 FT CHAIN 275 333 SPIKE GLYCOPROTEIN E3.
 FT CHAIN 334 756 SPIKE GLYCOPROTEIN E2.
 FT CHAIN 757 812 6 kDa PEPTIDE.
 FT CHAIN 813 1254 SPIKE GLYCOPROTEIN E1.
 FT ACT_SITE 151 151 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 157 157 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 225 225 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT TRANSMEM 701 721 POTENTIAL.
 FT TRANSMEM 794 813 POTENTIAL.
 FT TRANSMEM 1231 1248 POTENTIAL.
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 545 545 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 651 651 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 946 946 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1254 AA; 138343 MW; FB9DE88265F20211 CRC64;

Query Match 91.4%; Score 32; DB 1; Length 1254;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRGDC 5
 Db 1188 CKGDC 1192

Search completed: September 22, 2004, 06:52:12
 Job time : 25 secs

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RESULT 13
POLS_EEVV8
ID POLS_EEVV8 STANDARD; PRT; 1254 AA.
AC P05674;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Structural polyprotein (p130) [Contains: Coat protein C (EC 3.4.21.-)
DE (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
DE 6 kDa peptide; Spike glycoprotein E1].
OS Venezuelan equine encephalitis virus (strain TC-83).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=11037;
RN [1]
RX SEQUENCE FROM N.A. PubMed=3755750;
RA Johnson B.J.B., Kinney R.M., Kost C.L., Trent D.W.;
RT "Molecular determinants of alphavirus neurovirulence: nucleotide and
RT deduced protein sequence changes during attenuation of Venezuelan
RT equine encephalitis virus."
RL J. Gen. Virol. 67:1951-1960(1986).
CC -!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
CC -!- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
CC -!- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL
CC SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
CC HEMAGGLUTININ.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
CC -----
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CC -----
CC EMBL; X04368; CAA27883.1; -
CC PIR; A27871; VHWVE.
CC HSSP; P03315; IVCP.
CC MEROPS; S03.001; -
CC InterPro; IPR002548; Alpha_E1_glycop.
CC InterPro; IPR000936; Alpha_E2_glycop.
CC InterPro; IPR002533; Alpha_E3_glycop.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR000336; Flavi_glycoprote.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR000930; Peptidase_S3.
CC Pfam; PF00944; Alpha_core; 1.
CC Pfam; PF01589; Alpha_E1_glycop; 1.
CC Pfam; PF00943; Alpha_E2_glycop; 1.
CC Pfam; PF01563; Alpha_E3_glycop; 1.
CC PRINTS; PR00798; TOGAVIRIN.
CC Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
CC Serine protease.
FT CHAIN 1 275 COAT PROTEIN C.
FT CHAIN 276 SPIKE GLYCOPROTEIN E3.
FT CHAIN 335 SPIKE GLYCOPROTEIN E2.
FT CHAIN 758 6 kDa PEPTIDE.
FT CHAIN 813 SPIKE GLYCOPROTEIN E1.
FT ACT_SITE 152 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 158 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 226 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT TRANSMEM 702 POTENTIAL.
FT TRANSMEM 774 POTENTIAL.
FT TRANSMEM 792 POTENTIAL.
FT TRANSMEM 1231 POTENTIAL.
FT CARBOHYD 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 546 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 652 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 946 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1254 AA; 138485 MW; 7615698519A529F6 CRC64;
```

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Query Match 91.4%; Score 32; DB 1; Length 1254;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
DB 1188 CKGDC 1192

RESULT 14
POLS_EEVVE
ID POLS_EEVVE STANDARD; PRT; 1254 AA.
AC P36330; Q66582; Q66583; Q66584; Q66585; Q66586;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Structural polyprotein (P130) [Contains: Coat protein C (EC 3.4.21.-)
DE (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
DE 6 kDa peptide; Spike glycoprotein E1].
OS Venezuelan equine encephalitis virus (strain Everglades Fe3-7c).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=36383;
RN [1]
RX SEQUENCE FROM N.A. PubMed=8445371;
RA Snider J.M., Kinney R.M., Teuchiya K.R., Trent D.W.;
RT "Molecular evidence that epizootic Venezuelan equine encephalitis
RT (VEE) I-AB viruses are not evolutionary derivatives of enzootic VEE
RT subtype I-E or II viruses."
RL J. Gen. Virol. 74:519-523(1993).
CC -!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
CC -!- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
CC -!- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL
CC SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
CC HEMAGGLUTININ.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L04598; AAA42984.1; -
CC EMBL; L04598; AAA42983.1; ALT TERM.
CC EMBL; L04598; AAA42985.1; ALT SEQ.
CC EMBL; L04598; AAA42986.1; ALT SEQ.
CC EMBL; L04598; AAA42987.1; ALT SEQ.
CC EMBL; L04598; AAA42988.1; ALT_INIT.
CC PIR; JQ1978; JQ1978.
CC HSSP; P03315; IVCP.
CC MEROPS; S03.001; -
CC InterPro; IPR002548; Alpha_E1_glycop.
CC InterPro; IPR000936; Alpha_E2_glycop.
CC InterPro; IPR002533; Alpha_E3_glycop.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR000336; Flavi_glycoprote.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR000930; Peptidase_S3.
CC Pfam; PF00944; Alpha_core; 1.
CC Pfam; PF01589; Alpha_E1_glycop; 1.
CC Pfam; PF00943; Alpha_E2_glycop; 1.
CC Pfam; PF01563; Alpha_E3_glycop; 1.
CC PRINTS; PR00798; TOGAVIRIN.
CC Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
CC Serine protease.
FT CHAIN 1 274 COAT PROTEIN C.
FT CHAIN 275 SPIKE GLYCOPROTEIN E3.
FT CHAIN 334 SPIKE GLYCOPROTEIN E2.
```

RT "Nucleotide sequence of the genome region encoding the 26S mRNA of
 RT eastern equine encephalomyelitis virus and the deduced amino acid
 RT sequence of the viral structural proteins.";
 RL J. Gen. Virol. 68:2129-2142(1987).
 CC -!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
 CC -!- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
 CC -!- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL
 CC SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
 CC HEMAGGLUTININ.
 CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
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 CC -----
 CC EMBL; X05816; CAA29261.1; -;
 CC PIR; A26816; VHWVEE.
 CC HSP; P03315; 1VCP.
 CC MEROPS; S03.001; -;
 CC InterPro; IPR002548; Alpha_E1_glycop.
 CC InterPro; IPR000936; Alpha_E2_glycop.
 CC InterPro; IPR002533; Alpha_E3_glycop.
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR000336; Flavi_glycoprote.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR000930; Peptidase_S3.
 CC Pfam; PF00944; Alpha_core; 1.
 CC Pfam; PF01589; Alpha_E1_glycop; 1.
 CC Pfam; PF00943; Alpha_E2_glycop; 1.
 CC Pfam; PF01563; Alpha_E3_glycop; 1.
 CC PRINTS; PR00798; TOGAVIRIN.
 CC Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
 KW Serine protease.
 FT CHAIN 1 259 COAT PROTEIN C.
 FT CHAIN 260 322 SPIKE GLYCOPROTEIN E3.
 FT CHAIN 323 742 SPIKE GLYCOPROTEIN E2.
 FT CHAIN 743 798 6 kDa PEPTIDE.
 FT CHAIN 799 1239 SPIKE GLYCOPROTEIN E1.
 FT ACT_SITE 136 136 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 142 142 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 210 210 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT TRANSMEM 261 277 POTENTIAL.
 FT TRANSMEM 684 701 POTENTIAL.
 FT TRANSMEM 727 737 POTENTIAL.
 FT TRANSMEM 777 798 POTENTIAL.
 FT TRANSMEM 1211 1235 POTENTIAL.
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 932 932 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1239 AA; 137431 MW; 8C7664A05D2D41C CRC64;
 Query Match 91.4%; Score 32; DB 1; Length 1239;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 Db 1175 CKGDC 1179
 RESULT 12
 POLS_EEEV3
 ID POLS_EEEV3 STANDARD; PRT; 1240 AA.
 AC E27284;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Structural polyprotein (P130) [contains: Coat protein C (EC 3.4.21.-)
 DE (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;

DE 6 kDa peptide; Spike glycoprotein E1).
 OS Eastern equine encephalitis virus (strain va33[ten broeck]) (Eastern
 OS equine encephalomyelitis virus).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 OC Alphavirus.
 OX NCBI_TaxID=11022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91220727; PubMed=2024496;
 RA Weaver S.C., Scott T.W., Rico-Hesse R.;
 RT "Molecular evolution of eastern equine encephalomyelitis virus in
 RT North America";
 RL Virology 182:774-784(1991).
 CC -!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
 CC -!- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
 CC -!- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL
 CC SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
 CC HEMAGGLUTININ.
 CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
 CC -----
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 CC -----
 CC EMBL; M69094; AAA42980.1; -;
 CC PIR; A39992; VHWVEV.
 CC HSP; P03315; 1VCP.
 CC MEROPS; S03.001; -;
 CC InterPro; IPR002548; Alpha_E1_glycop.
 CC InterPro; IPR000936; Alpha_E2_glycop.
 CC InterPro; IPR002533; Alpha_E3_glycop.
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR000336; Flavi_glycoprote.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR000930; Peptidase_S3.
 CC Pfam; PF00944; Alpha_core; 1.
 CC Pfam; PF01589; Alpha_E1_glycop; 1.
 CC Pfam; PF00943; Alpha_E2_glycop; 1.
 CC Pfam; PF01563; Alpha_E3_glycop; 1.
 CC PRINTS; PR00798; TOGAVIRIN.
 CC Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
 KW Serine protease.
 FT CHAIN 1 260 COAT PROTEIN C.
 FT CHAIN 261 323 SPIKE GLYCOPROTEIN E3.
 FT CHAIN 324 743 SPIKE GLYCOPROTEIN E2.
 FT CHAIN 744 799 6 kDa PEPTIDE.
 FT CHAIN 800 1240 SPIKE GLYCOPROTEIN E1.
 FT ACT_SITE 137 137 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 143 143 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 211 211 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT TRANSMEM 259 276 POTENTIAL.
 FT TRANSMEM 695 712 POTENTIAL.
 FT TRANSMEM 722 738 POTENTIAL.
 FT TRANSMEM 781 799 POTENTIAL.
 FT TRANSMEM 1212 1236 POTENTIAL.
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 834 834 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 933 933 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1240 AA; 137290 MW; AEBEB1599D083045 CRC64;
 Query Match 91.4%; Score 32; DB 1; Length 1240;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 Db 1176 CKGDC 1180

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FT METAL 256 256 IRON 1 (BY SIMILARITY).
FT METAL 394 394 IRON 2 (BY SIMILARITY).
FT METAL 429 429 IRON 2 (BY SIMILARITY).
FT METAL 524 524 IRON 2 (BY SIMILARITY).
FT METAL 592 592 IRON 2 (BY SIMILARITY).
FT BINDING 128 128 CARBONATE 1 (BY SIMILARITY).
FT BINDING 132 132 CARBONATE 1 (BY SIMILARITY).
FT BINDING 134 134 CARBONATE 1 (VIA AMIDE NITROGEN) (BY
FT BINDING 135 135 SIMILARITY).
FT BINDING 135 135 CARBONATE 1 (VIA AMIDE NITROGEN) (BY
FT BINDING 454 454 CARBONATE 2 (BY SIMILARITY).
FT BINDING 458 458 CARBONATE 2 (BY SIMILARITY).
FT BINDING 460 460 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
FT BINDING 461 461 SIMILARITY).
FT BINDING 461 461 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
FT SEQUENCE 690 AA; 74600 MW; 2F996CALAE79570 CRC64;

Query Match 91.4%; Score 32; DB 1; Length 690;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 185 CKGDC 189

RESULT 10
TRF2_SALSA STANDARD; PRT; 691 AA.
AC PR0429;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serotransferrin II precursor (Siderophilin II) (STF II).
GN STF2.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=9412797; PubMed=8293074;
RA Kvingedal A.M., Roervik K.A., Alestroem P.;
RT "Cloning and characterization of Atlantic salmon (Salmo salar) serum
RT transferrin cDNA.";
RL Mol. Mar. Biol. Biotechnol. 2:233-238(1993).
RN [2]
RP SEQUENCE OF 19-37.
RC TISSUE=Serum;
RA Røed K.H., Dehli A.K., Fløngsrud R., Midtjell L., Roervik K.A.;
RT "Immunoassay and partial characterization of serum transferrin from
RT Atlantic salmon (Salmo salar L.).";
RL Fish Shellfish Immunol. 5:71-80(1995).
CC -!- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Abundant in liver and serum with smaller
CC amounts found in the stomach and kidney.
CC -!- DOMAIN: Composed of two homologous domains.
CC -!- SIMILARITY: Belongs to the transferrin family.
HSSP; P56410; IAOV.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.

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DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
Signal.
FT CHAIN 1 18 SEROTRANSFERRIN II.
FT DISULFID 19 691 BY SIMILARITY.
FT DISULFID 28 50 BY SIMILARITY.
FT DISULFID 127 207 BY SIMILARITY.
FT DISULFID 172 186 BY SIMILARITY.
FT DISULFID 235 249 BY SIMILARITY.
FT DISULFID 343 379 BY SIMILARITY.
FT DISULFID 353 370 BY SIMILARITY.
FT DISULFID 404 682 BY SIMILARITY.
FT DISULFID 419 643 BY SIMILARITY.
FT DISULFID 451 530 BY SIMILARITY.
FT DISULFID 475 671 BY SIMILARITY.
FT DISULFID 485 499 BY SIMILARITY.
FT DISULFID 496 513 BY SIMILARITY.
FT DISULFID 570 584 BY SIMILARITY.
FT METAL 74 74 IRON 1 (BY SIMILARITY).
FT METAL 104 104 IRON 1 (BY SIMILARITY).
FT METAL 201 201 IRON 1 (BY SIMILARITY).
FT METAL 257 257 IRON 1 (BY SIMILARITY).
FT METAL 394 394 IRON 2 (BY SIMILARITY).
FT METAL 428 428 IRON 2 (BY SIMILARITY).
FT METAL 524 524 IRON 2 (BY SIMILARITY).
FT METAL 592 592 IRON 2 (BY SIMILARITY).
FT CARBOHYD 169 169 N-LINKED (GLCNAC...) (POTENTIAL).
FT BINDING 129 129 CARBONATE 1 (BY SIMILARITY).
FT BINDING 134 134 CARBONATE 1 (VIA AMIDE NITROGEN) (BY
FT BINDING 136 136 SIMILARITY).
FT BINDING 137 137 CARBONATE 1 (VIA AMIDE NITROGEN) (BY
FT BINDING 453 453 CARBONATE 2 (BY SIMILARITY).
FT BINDING 457 457 CARBONATE 2 (BY SIMILARITY).
FT BINDING 459 459 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
FT BINDING 460 460 SIMILARITY).
FT BINDING 460 460 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
FT SEQUENCE 691 AA; 74663 MW; 8D2431663677CF2D CRC64;

Query Match 91.4%; Score 32; DB 1; Length 691;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 186 CKGDC 190

RESULT 11
POL_S_EEEV STANDARD; PRT; 1239 AA.
AC PR0768;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Structural polyprotein (Pl30) [Contains: Coat protein C (EC 3.4.21.-)
DE (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
DE 6 kDa peptide; Spike glycoprotein E1].
OS Eastern equine encephalitis virus (Eastern equine encephalomyelitis
OS virus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=11021;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=82V-2137;
RX MEDLINE=87282265; PubMed=2886548;
RX Chang G.-J.J., Trent D.W.;

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of an anion, usually bicarbonate. It is responsible for the transport of iron from sites of absorption and heme degradation to those of storage and utilization. Serum transferrin may also have a further role in stimulating cell proliferation.

-!- SUBUNIT: Monomer.

-!- SURCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Abundant in liver and serum with smaller amounts found in the stomach and kidney.

-!- DOMAIN: Composed of two homologous domains.

-!- SIMILARITY: Belongs to the transferrin family.

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EMBL; L20313; AAA18838.1; -
 EMBL; L26909; AAC42221.1; -
 PIR; I51350; I51350.
 PIR; T11749; T11749.
 HSSP; P56410; LAOV.
 InterPro; IPR001156; Transferrin.
 Pfam; PF00405; transferrin; 2.
 PRINTS; PR00422; TRANSFERRIN.
 SMART; SM00094; TR FER; 2.
 PROSITE; PS00205; TRANSFERRIN_1; 2.
 PROSITE; PS00206; TRANSFERRIN_2; 2.
 PROSITE; PS00207; TRANSFERRIN_3; 1.
 Transprot; Iron transport; Glycoprotein; Metal-binding; Repeat;
 Signal.

FT	CHAIN	1	18	SEROTRANSFERRIN I.
FT	DISULFID	19	690	BY SIMILARITY.
FT	DISULFID	28	50	BY SIMILARITY.
FT	DISULFID	127	207	BY SIMILARITY.
FT	DISULFID	172	186	BY SIMILARITY.
FT	DISULFID	235	249	BY SIMILARITY.
FT	DISULFID	343	379	BY SIMILARITY.
FT	DISULFID	353	370	BY SIMILARITY.
FT	DISULFID	404	681	BY SIMILARITY.
FT	DISULFID	404	681	BY SIMILARITY.
FT	DISULFID	419	642	BY SIMILARITY.
FT	DISULFID	451	529	BY SIMILARITY.
FT	DISULFID	475	670	BY SIMILARITY.
FT	DISULFID	485	499	BY SIMILARITY.
FT	DISULFID	496	512	BY SIMILARITY.
FT	DISULFID	529	533	BY SIMILARITY.
FT	METAL	74	74	IRON 1 (BY SIMILARITY).
FT	METAL	104	104	IRON 1 (BY SIMILARITY).
FT	METAL	201	201	IRON 1 (BY SIMILARITY).
FT	METAL	257	257	IRON 1 (BY SIMILARITY).
FT	METAL	394	394	IRON 2 (BY SIMILARITY).
FT	METAL	428	428	IRON 2 (BY SIMILARITY).
FT	METAL	523	523	IRON 2 (BY SIMILARITY).
FT	METAL	591	591	IRON 2 (BY SIMILARITY).
FT	CARBOHYD	169	169	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	BINDING	129	129	CARBONATE 1 (BY SIMILARITY).
FT	BINDING	134	134	CARBONATE 1 (BY SIMILARITY).
FT	BINDING	136	136	CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT	BINDING	137	137	CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT	BINDING	453	453	CARBONATE 2 (BY SIMILARITY).
FT	BINDING	457	457	CARBONATE 2 (BY SIMILARITY).
FT	BINDING	459	459	CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT	BINDING	460	460	CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT	CONFLICT	34	34	E -> Q (IN REF. 3).
SQ	SEQUENCE	690 AA;	74597 MW;	D1F4FC7A6AFA3FB CRC64;

Query Match 91.4%; Score 32; DB 1; Length 690;

Best Local Similarity 80.0%; Pred. No. 64;
 Matches 4; Conservative 1; Mismatches 0; Gaps 0;

Qy	1	CRGDC 5	Indels	0;
Db	186	CKGDC 190		

RESULT 9

ID	TRFE ORYLA	STANDARD;	PRT;	690 AA.
AC	P79819			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Serotransferrin precursor.			
OS	Oryzias latipes (Medaka fish) (Japanese ricefish).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;			
OC	Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.			
OX	NCBI TaxID=8090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96414927; PubMed=8817928;			
RA	Mikawa N., Hirono I., Aoki T.;			
RT	"Structure of medaka transferrin gene and its 5'-flanking region.";			
RL	Mol. Mar. Biol. Biotechnol. 5:225-229(1996).			
CC	-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.			
CC	-!- SUBUNIT: Monomer (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- DOMAIN: Composed of two homologous domains.			
CC	-!- SIMILARITY: Belongs to the transferrin family.			
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CC	EMBL; D64033; BAA10301.1; -			
DR	HSSP; P56410; LAOV.			
DR	InterPro; IPR001156; Transferrin.			
DR	Pfam; PF00405; transferrin; 2.			
DR	PRINTS; PR00422; TRANSFERRIN.			
DR	SMART; SM00094; TR FER; 2.			
DR	PROSITE; PS00205; TRANSFERRIN_1; 2.			
DR	PROSITE; PS00206; TRANSFERRIN_2; 2.			
DR	PROSITE; PS00207; TRANSFERRIN_3; FALSE NEG.			
KW	Transprot; Iron transport; Glycoprotein; Metal-binding; Repeat;			
KW	Signal.			
FT	CHAIN	1	17	BY SIMILARITY.
FT	DISULFID	18	690	SEROTRANSFERRIN.
FT	DISULFID	27	49	BY SIMILARITY.
FT	DISULFID	126	206	BY SIMILARITY.
FT	DISULFID	171	185	BY SIMILARITY.
FT	DISULFID	234	248	BY SIMILARITY.
FT	DISULFID	343	379	BY SIMILARITY.
FT	DISULFID	353	370	BY SIMILARITY.
FT	DISULFID	404	682	BY SIMILARITY.
FT	DISULFID	419	643	BY SIMILARITY.
FT	DISULFID	452	530	BY SIMILARITY.
FT	DISULFID	476	671	BY SIMILARITY.
FT	DISULFID	486	499	BY SIMILARITY.
FT	DISULFID	496	513	BY SIMILARITY.
FT	DISULFID	570	584	BY SIMILARITY.
FT	METAL	73	73	IRON 1 (BY SIMILARITY).
FT	METAL	103	103	IRON 1 (BY SIMILARITY).
FT	METAL	200	200	IRON 1 (BY SIMILARITY).

RT factor-beta superfamily containing a novel pattern of cysteines.";
 RL J. Biol. Chem. 268:3444-3449(1993).
 CC -!- FUNCTION: REQUIRED FOR OVARIAN FOLLICULOGENESIS.
 CC -!- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL). BUT, IN CONTRAST TO
 CC OTHER MEMBERS OF THIS FAMILY, CANNOT BE DISULFIDE-LINKED.
 CC -!- TISSUE SPECIFICITY: Ovary.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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 CC -----
 DR EMBL; L06444; AAA53035.1; -
 DR PIR; S45284; S45284.
 DR HSSP; PI2643; 3BMP.
 DR MGD; MGI:95692; Gdf9.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR Pfam; PF00019; TGF-beta; 1.
 DR PRINTS; PR00669; INHIBINA.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 306 POTENTIAL.
 FT CHAIN 307 441 GROWTH/DIFFERENTIATION FACTOR 9.
 FT DISULFID 340 406 BY SIMILARITY.
 FT DISULFID 369 438 BY SIMILARITY.
 FT DISULFID 373 440 BY SIMILARITY.
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 441 AA; 49636 MW; E27071359B899C3C CRC64;
 Query Match 91.4%; Score 32; DB 1; Length 441;
 Best Local Similarity 80.0%; Pred. No. 42;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 Db 369 CRGDC 373
 RESULT 5
 GDF9 SHEEP
 ID GDF9 SHEEP STANDARD; PRT; 453 AA.
 AC O77681;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Growth/differentiation factor 9 precursor (GDF-9).
 GN GDF9.
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99115226; PubMed-9916005;
 RA Bodensteiner K.J., Clay C.M., Moeller C.L., Sawyer H.R.;
 RT "Molecular cloning of the ovine Growth/Differentiation factor-9 gene
 RT and expression of growth/differentiation factor-9 in ovine and bovine
 RT ovaries."
 RL Biol. Reprod. 60:381-386(1999).
 CC -!- FUNCTION: REQUIRED FOR OVARIAN FOLLICULOGENESIS.
 CC -!- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL). BUT, IN CONTRAST TO

CC OTHER MEMBERS OF THIS FAMILY, CANNOT BE DISULFIDE-LINKED (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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 CC -----
 DR EMBL; AF078545; AAC28089.2; -
 DR HSSP; PI2643; 3BMP.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR Pfam; PF00019; TGF-beta; 1.
 DR PRINTS; PR00669; INHIBINA.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 27 POTENTIAL.
 FT PROPEP 28 318 POTENTIAL.
 FT CHAIN 319 453 GROWTH/DIFFERENTIATION FACTOR 9.
 FT DISULFID 352 418 BY SIMILARITY.
 FT DISULFID 381 450 BY SIMILARITY.
 FT DISULFID 385 452 BY SIMILARITY.
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 453 AA; 51776 MW; 1911A66A720E2B85 CRC64;
 Query Match 91.4%; Score 32; DB 1; Length 453;
 Best Local Similarity 80.0%; Pred. No. 44;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 Db 381 CRGDC 385
 RESULT 6
 GDF9 HUMAN
 ID GDF9 HUMAN STANDARD; PRT; 454 AA.
 AC O60383;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Growth/differentiation factor 9 precursor (GDF-9).
 GN GDF9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kimmerly W., Bondoc M., Cheng J., Connolly K.S., Gunning K.M.,
 RA Davis C.A., Kadner K., Miguel T., Pitluck S., Pollard M., Rojeski H.,
 RA Subramanian S., Martin C.H.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: REQUIRED FOR OVARIAN FOLLICULOGENESIS.
 CC -!- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL). BUT, IN CONTRAST TO
 CC OTHER MEMBERS OF THIS FAMILY, CANNOT BE DISULFIDE-LINKED (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF BETA.1; 1.
KW Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 ?
FT PROPEP ? 833
FT CHAIN 834 946
FT DOMAIN 21 50
FT INHIBIN BETA CHAIN.
FT CYS-RICH.
FT ARG-RICH.
FT BY SIMILARITY.
FT DISULFID 837 846
FT DISULFID 845 912
FT DISULFID 874 943
FT DISULFID 878 945
FT DISULFID 911 911
FT CARBOHYD 208 208
FT CARBOHYD 217 217
FT CARBOHYD 271 271
FT CARBOHYD 389 389
FT CARBOHYD 471 471
FT CARBOHYD 484 484
FT CARBOHYD 542 542
FT CARBOHYD 561 561
FT CARBOHYD 566 566
FT CARBOHYD 732 732
FT CARBOHYD 804 804
FT CARBOHYD 275 275
FT CONFLICT 517 517
FT CONFLICT I -> T (IN REF. 4).
FT CONFLICT I -> V (IN REF. 4).
SQ SEQUENCE 946 AA; 108791 MW; 7CECD6E73EAA306B CRC64;

Query Match 100.0%; Score 35; DB 1; Length 946;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 874 CRGDC 878

RESULT 3
MTL_CABEL STANDARD; PRT; 74 AA.
AC P17511;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metallothionein-I (MT-I).
GN MT-I OR MET-I OR K11G9.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90094407; PubMed=2294106;
RA Slice L.W., Freedman J.H., Rubin C.S.;
RT "Purification, characterization, and cDNA cloning of a novel
RT metallothionein-like, cadmium-binding protein from Caenorhabditis
RT elegans."
RL J. Biol. Chem. 265:256-263 (1990).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-24.
RC STRAIN=Bristol N2;
RX MEDLINE=90262552; PubMed=2344361;
RA Imagawa M., Onozawa T., Okumura K., Osada S., Nishihara T., Kondo M.;
RT "Characterization of metallothionein cDNAs induced by cadmium in the
RT nematode Caenorhabditis elegans."
RL Biochem. J. 268:237-240 (1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93155063; PubMed=8428932;

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RA Freedman J.H., Slice L.W., Dixon D., Fire A., Rubin C.S.;
RT "The novel metallothionein genes of Caenorhabditis elegans.
RT Structural organization and inducible, cell-specific expression."
RL J. Biol. Chem. 268:2554-2564 (1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=95151184; PubMed=7848551;
RA Kugawa F., Yamamoto H., Osada S., Aoki M., Imagawa M., Nishihara T.;
RT "Metallothionein genes in the nematode Caenorhabditis elegans and
RT metal inducibility in mammalian culture cells."
RL Biomed. Environ. Sci. 7:222-231 (1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX STRAIN=Bristol N2;
RA Greco T., Bradshaw H.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN BINDS CATIONS OF SEVERAL TRANSITION
CC ELEMENTS.
CC -1- INDUCTION: By cadmium.
CC -1- DOMAIN: ALL CYSTEINE RESIDUES ARE ARRANGED IN C-X-C GROUPS. THESE
CC ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER
CC METALLOTHIONEINS.
CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 6.
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; M92909; AAA28110.1; -
CC EMBL; X53244; CAA37334.1; -
CC EMBL; D17364; BAA04180.1; -
CC EMBL; U64853; AAB04979.1; -
CC DR PIR; B45206; B45206.
CC DR WormPep; K11G9.6; CE07379.
CC DR InterPro; IPR000853; Mclthion_nemat.
CC PRINTS; PR00876; MTNEMATODE.
KW Metal-binding; Metal-thiolate cluster; Cadmium.
FT INIT_MET 0
FT CONFLICT 22 22 D -> G (IN REF. 2; AA SEQUENCE).
SQ SEQUENCE 74 AA; 7959 MW; DA0D0C9FD6240C3 CRC64;

Query Match 91.4%; Score 32; DB 1; Length 74;
Best Local Similarity 80.0%; Pred. No. 8.4;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 43 CRGDC 47

RESULT 4
GDF9 MOUSE STANDARD; PRT; 441 AA.
ID_GDF9_MOUSE STANDARD; PRT; 441 AA.
AC Q07103;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Growth/differentiation factor 9 precursor (GDF-9).
GN GDF9 OR GDF-9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93155193; PubMed=8429021;
RA McPherron A.C., Lee S.-J.;
RT "GDF-3 and GDF-9: two new members of the transforming growth

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DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PRO0438; GFCYSKNOT.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF BETA 1; 1.
KW Growth factor; Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 234
FT CHAIN 235 350
FT
FT DISULFID 241 251
FT DISULFID 250 315
FT DISULFID 278 347
FT DISULFID 282 349
FT DISULFID 314 314
FT CARBOHYD 23 23
FT MUTAGEN 271 271
FT MUTAGEN 280 280
SQ SEQUENCE 350 AA; 39533 MW; F957C70A2B1FDE0A CRC64;
Query Match 100.0%; Score 35; DB 1; Length 350;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDC 5
DB 278 CRGDC 282
|||||
RESULT 2
ID IHB_DROME STANDARD; PRT; 946 AA.
AC 061643; QSMRBI; QSMR60; Q9VA97;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Inhibin beta chain precursor (Activin beta chain).
GN ACTIVIN-BETA OR CG1062.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA De Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fodor C.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster G., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hosin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.C., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RN [2]
RP REVISIONS.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley; TISSUE=Embryo;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
RN [4]
RP SEQUENCE OF 209-946 FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22090541; PubMed=12095682;
RA Haery T.E., O'Connor M.B.;
RT "Isolation of Drosophila activin and follistatin cDNAs using novel
RT MACH amplification protocols.";
RL Gene 291:85-93(2002).
RN [5]
RP SEQUENCE OF 574-946 FROM N.A., AND DEVELOPMENTAL STAGE.
RX MEDLINE=98289585; PubMed=9618266;
RA Kuty G., Kuty R.K., Samuel W., Duncan T., Jaworski C., Wiggert B.;
RT "Identification of a new member of transforming growth factor-beta
RT superfamily in Drosophila: the first invertebrate activin gene.";
RL Biochem. Biophys. Res. Commun. 246:644-649(1998).
CC -!- SUBUNIT: Homodimer or heterodimer; disulfide-linked (Potential).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- DEVELOPMENTAL STAGE: Expressed in embryonic, larval and adult
CC stages.
CC -!- SIMILARITY: Belongs to the TGF-beta family.
CC
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CC
CC EMBL; AE003846; AAF59386.3; -
CC EMBL; AY121686; AAM52013.1; -
CC EMBL; AF454392; AAL51005.1; -
CC EMBL; AF054822; AAC39083.1; -
CC HSSP; P18075; 1BMP.
CC
CC FlyBase; FBgn0024913; activin-beta.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0005160; P:transforming growth factor-beta receptor bi. . .; NAS.
CC GO; GO:0016049; P:cell growth; NAS.
CC InterPro; IPR002405; Inhibin_alpha.

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OM protein - protein search, using sw model

Run on: September 22, 2004, 06:39:36 ; Search time 23 Seconds
(without alignments)
11.320 Million cell updates/sec

Title: US-09-912-609-9

Perfect score: 35
Sequence: 1 CRGDC 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	350	1	DAF7 CAEEL
2	35	100.0	946	1	IHB_DROME
3	32	91.4	74	1	MTL_CAEEL
4	32	91.4	441	1	GDF9_MOUSE
5	32	91.4	453	1	GDF9_SHEEP
6	32	91.4	454	1	GDF9_HUMAN
7	32	91.4	654	1	BGLX_BRWCH
8	32	91.4	690	1	TRF1_SALSA
9	32	91.4	690	1	TRF2_ORYLA
10	32	91.4	691	1	TRF2_SALSA
11	32	91.4	1239	1	POL5_EEEV
12	32	91.4	1240	1	POL5_EEEV3
13	32	91.4	1254	1	POL5_EEEV8
14	32	91.4	1254	1	POL5_EEEV2
15	32	91.4	1254	1	POL5_EEEVM
16	32	91.4	1254	1	POL5_EEEVT
17	32	91.4	1255	1	POL5_EEEV3
18	32	91.4	1255	1	POL5_EEEV3
19	30	85.7	72	1	CHHA_CHEDE
20	30	85.7	95	1	Y117_NPVAC
21	30	85.7	101	1	VE7_HPV21
22	30	85.7	102	1	VE7_HPV19
23	30	85.7	102	1	VE7_HPV20
24	30	85.7	102	1	VE7_HPV25
25	30	85.7	102	1	VE7_HPV36
26	30	85.7	103	1	VE7_HPV05
27	30	85.7	103	1	VE7_HPV08
28	30	85.7	103	1	VE7_HPV12
29	30	85.7	103	1	VE7_HPV47
30	30	85.7	103	1	VE7_HPV5B
31	30	85.7	344	1	GUN4_TRIRE
32	30	85.7	401	1	BMP4_XENLA
33	30	85.7	405	1	BMP4_CHICK

ALIGNMENTS

RESULT 1
DAF7 CAEEL
ID DAF7 CAEEL STANDARD; PRT; 350 AA.
AC P92172;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Dauer larva development regulatory growth factor daf-7 precursor
DE (Abnormal dauer formation protein 7).
GN DAF-7 OR B0412.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
OC Rhabditiidae; Peloderinae; Caenorhabditis.
ON NCBI_TaxID=6239;
RX MEDLINE=97067238; PubMed=8910282;
RA Ren P., Lim C.-S., Johnson R., Albert P.S., Pilgrim D., Riddle D.L.;
RT "Control of C. elegans larval development by neuronal expression of a
TGF-beta homolog.";
RL Science 274:1389-1391 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May act as a negative regulator of dauer larva
development by transducing chemosensory information from ASI
neurons.
CC -!- TISSUE SPECIFICITY: Expression in the chemosensory neurons.
CC -!- DEVELOPMENTAL STAGE: WHEN THE FOOD/PHEROMONE RATIO IS HIGH, ITS
LEVEL PEAKS DURING THE L1 LARVAL STAGE. EXPRESSION IS DETECTED IN
LARVAE BEGINNING 4 TO 5 HOURS AFTER HATCHING, THROUGH THE FOUR
LARVAL STAGES, AND IN ADULTS
CC -!- INDUCTION: Dauer-inducing pheromone inhibits its expression and
promotes dauer formation, whereas food reactivates its expression
and promotes recovery from the dauer state.
CC -!- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC -----
CC EMBL; U72883; AAC47390.1; -;
CC EMBL; U72884; AAC47389.1; -;
CC EMBL; U80953; AAB52554.1; -;
CC PIR; T25451; T25451.
CC HGSP; P12643; 3BMP.
CC WormPep; B0412.2; CE01758.
CC InterPro; IPR002400; GFCysknot.
CC InterPro; IPR001839; TGFb.
CC -----

34 30 85.7 408 1 BMP4 DAMDA
35 30 85.7 408 1 BMP4_HUMAN
36 30 85.7 408 1 BMP4_MOUSE
37 30 85.7 408 1 BMP4_RAT
38 30 85.7 409 1 BMP4_RABIT
39 30 85.7 551 1 ARS_HEMPU
40 30 85.7 567 1 ARS_STRPU
41 30 85.7 1233 1 MU5A_HUMAN
42 30 85.7 1884 1 RRPO_ACLSP
43 30 85.7 1885 1 RRPO_ACLSA
44 29 82.9 25 1 CXOB_CONCT
45 29 82.9 83 1 VIH_ARMVU

Q29607 dama dama (
P12644 homo sapien
P21275 mus musculu
Q05826 rattus norv
O46576 oryctolagus
P14000 hemicephal
P50473 stronglylce
P98088 homo sapien
P27738 apple chlor
P54891 apple chlor
P58918 conus catus
P83627 armadillidi

```

RESULT 12
VHWVEE
structural polyprotein - eastern equine encephalomyelitis virus (strain 82V-2137)
N:Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein
C:Species: eastern equine encephalomyelitis virus
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Jul-1999
C:Accession: A26816
R:Chang, G.J.J.; Trent, D.W.
J. Gen. Virol. 68, 2125-2142, 1987
A:Title: Nucleotide sequence of the genome region encoding the 26S mRNA of eastern equine
A:Reference number: A26816; MUID:87282265; PMID:2886548
A:Accession: A26816
A:Molecule type: mRNA
A:Residues: 1-1239 <CHA>
A:Cross-references: EMBL:X05816; NID:G62074; PIDN:CAA29261.1; PID:G62075
C:Superfamily: togavirus structural polyprotein
C:Keywords: coat protein; glycoprotein; transmembrane protein
F:1-259/Product: coat protein C #status predicted <CPC>
F:260-322/Product: membrane glycoprotein E3 #status predicted <MG3>
F:323-742/Product: transmembrane #status predicted <TN1>
F:727-737/Product: membrane glycoprotein E2 #status predicted <MG2>
F:727-737/Product: transmembrane #status predicted <TN2>
F:727-737/Product: transmembrane #status predicted <TN3>
F:743-798/Product: 6K protein #status predicted <K6P>
F:777-798/Product: transmembrane #status predicted <TN4>
F:799-1239/Product: membrane glycoprotein E1 #status predicted <MG1>
F:1211-1235/Domain: transmembrane #status predicted <TN5>
F:49,270,624,637,932/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          91.4%; Score 32; DB 1; Length 1239;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
    |:|||
Db 1175 CKGDC 1179

RESULT 13
VHWVEE
structural polyprotein - eastern equine encephalomyelitis virus (strain VA33[Ten Broeck])
N:Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein
C:Species: eastern equine encephalomyelitis virus
A:Note: host Equus caballus (domestic horse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C:Accession: A39992
R:Weaver, S.C.; Scott, T.W.; Rico-Hesse, R.
Virology 182, 774-784, 1991
A:Title: Molecular evolution of eastern equine encephalomyelitis virus in North America.
A:Reference number: A39992; MUID:91220727; PMID:2024496
A:Accession: A39992
A:Molecule type: genomic RNA
A:Residues: 1-1240 <WEA>
A:Cross-references: GB:M69094; NID:G323696; PIDN:AAA42980.1; PID:G323697
A:Note: the authors translated the codon AGC for residue 836 as Arg and GUU for residue
C:Superfamily: togavirus structural polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-260/Product: coat protein C #status predicted <CPC>
F:259-276/Domain: transmembrane #status predicted <TN1>
F:261-323/Product: membrane glycoprotein E3 #status predicted <EG3>
F:324-743/Product: membrane glycoprotein E2 #status predicted <EG2>
F:695-712/Domain: transmembrane #status predicted <TN2>
F:722-738/Domain: transmembrane #status predicted <TN3>
F:744-799/Product: 6K protein #status predicted <K6P>
F:781-799/Domain: transmembrane #status predicted <TN4>
F:800-1240/Product: membrane glycoprotein E1 #status predicted <EG1>
F:1212-1236/Domain: transmembrane #status predicted <TN5>
F:49,271,625,834,933/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          91.4%; Score 32; DB 1; Length 1240;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
    |:|||
Db 1175 CKGDC 1179

```

```

QY 1 CRGDC 5
    |:|||
Db 1176 CKGDC 1180

RESULT 14
S26373
genome polyprotein - eastern equine encephalomyelitis virus
N:Contains: 6K protein; capsid protein C; envelope protein E1; envelope protein E2; envel
C:Species: eastern equine encephalomyelitis virus
C:Date: 06-Jan-1994 #sequence_revision 01-Nov-1996 #text_change 26-Aug-1999
C:Accession: S26373
R:Volchkov, V.E.; Volchkova, V.A.; Netesov, S.V.
Mol. Gen. Microbiol. Virusol. 5, 8-15, 1991
A:Title: Complete nucleotide sequence of the eastern equine encephalomyelitis virus gen
A:Reference number: S26369; MUID:91375524; PMID:1896061
A:Accession: S26373
A:Molecule type: mRNA
A:Residues: 1-1241 <VOL>
A:Cross-references: EMBL:X63135; NID:G59185; PIDN:CAA44845.1; PID:G59186
A:Note: sequence could not be checked because of bad print in paper
C:Superfamily: togavirus structural polyprotein
C:Keywords: capsid protein; envelope protein; glycoprotein; polyprotein
F:1-260/Product: capsid protein C #status predicted <CAP>
F:261-323/Product: envelope protein E3 #status predicted <EP3>
F:324-743/Product: envelope protein E2 #status predicted <EP2>
F:744-800/Product: 6K protein #status predicted <K6P>
F:801-1241/Product: envelope protein E1 #status predicted <EP1>

Query Match          91.4%; Score 32; DB 2; Length 1241;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
    |:|||
Db 1177 CKGDC 1181

RESULT 15
S72350
structural polyprotein - eastern equine encephalomyelitis virus
N:Contains: 6K protein; capsid protein; E1 protein; E2 protein; E3 protein
C:Species: eastern equine encephalomyelitis virus
C:Date: 04-May-1998 #sequence_revision 15-May-1998 #text_change 26-Aug-1999
C:Accession: S72350
R:Weaver, S.C.; Hagenbaugh, A.; Bellew, L.A.; Netesov, S.V.; Volchkov, V.E.; Chang, G.J.
Virology 197, 375-390, 1993
A:Title: A comparison of the nucleotide sequences of eastern and western equine encephal
A:Reference number: S72349; MUID:94025587; PMID:8105605
A:Accession: S72350
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-1242 <WEA>
A:Cross-references: EMBL:U01034; NID:G393006; PIDN:AAC53735.1; PID:G393008
C:Superfamily: togavirus structural polyprotein

Query Match          91.4%; Score 32; DB 2; Length 1242;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
    |:|||
Db 1178 CKGDC 1182

Search completed: September 22, 2004, 06:52:57
Job time : 41 secs

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hypothetical protein AT4g09620 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
 C;Accession: D85098
 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
 A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A;Reference number: A85001; MUID:20083488; PMID:10617198
 A;Accession: D85098
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-210 <STO>
 A;Cross-references: GB:NC_001268; NID:G7267657; PIDN:CAB78085.1; GSPDB:GN00140
 C;Genetics:
 A;Gene: AT4g09620
 A;Map position: 4

Query Match
 Best Local Similarity 91.4%; Score 32; DB 2; Length 210;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 Db 195 CKGDC 199
 |||||

RESULT 8
 S45284
 growth/differentiation factor GDF-9 precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1993 #sequence_revision 20-Feb-1995 #text_change 17-Mar-2000
 C;Accession: S45284; B46607
 R;Incerti, B.; Dong, J.; Borsani, G.; Matzuk, M.M.
 Biochim. Biophys. Acta 1222, 125-128, 1994
 A;Title: Structure of the mouse growth/differentiation factor 9 gene.
 A;Reference number: S45284; MUID:94242792; PMID:8186260
 A;Accession: S45284
 A;Molecule type: DNA
 A;Residues: 1-441 <INC>
 A;Cross-references: EMBL:X77112
 A;Experimental source: ovary, strain 129SvEv (Stratagene)
 R;McPherron, A.C.; Lee, S.J.
 J. Biol. Chem. 268, 3444-3449, 1993
 A;Title: GDF-3 and GDF-9: two new members of the transforming growth factor-beta superfamily
 A;Reference number: A46607; MUID:93155193; PMID:8429021
 A;Accession: B46607
 A;Molecule type: mRNA
 A;Residues: 1-295; T, 297-441 <MCP>
 A;Cross-references: GB:L06444; NID:9293348; PIDN:AAA53035.1; PID:G567206
 A;Experimental source: ovary
 C;Genetics:
 A;Introns: 133/1
 C;Superfamily: inhibin
 C;Keywords: growth factor; ovary

Query Match
 Best Local Similarity 91.4%; Score 32; DB 2; Length 441;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 Db 369 CKGDC 373
 |||||

RESULT 9
 S53805
 beta-glucosidase/xylosidase - Erwinia chrysanthemi
 C;Species: Erwinia chrysanthemi
 C;Date: 27-Oct-1995 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
 C;Accession: S53805
 R;Vroemen, S.; Heldens, J.; Boyd, C.; Henrissat, B.; Keen, N.T.
 Mol. Gen. Genet. 246, 465-477, 1995
 A;Title: Cloning and characterization of the bgxA gene from Erwinia chrysanthemi D1 whid

A;Reference number: S53805; MUID:95198684; PMID:7891660
 A;Accession: S53805
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-654 <VRO>

Query Match
 Best Local Similarity 91.4%; Score 32; DB 2; Length 654;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 Db 367 CKGDC 371
 |||||

RESULT 10
 T11749
 transferrin - Atlantic salmon
 C;Species: Salmo salar (Atlantic salmon)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C;Accession: T11749
 R;Kvingedal, A.M.; Rorvik, K.A.; Alestrom, P.
 Mol. Marine Biol. Biotechnol. 2, 233-238, 1993
 A;Title: Cloning and characterization of Atlantic salmon (Salmo salar) serum transferrin
 A;Reference number: Z17332; MUID:94122797; PMID:8253074
 A;Accession: T11749
 A;Status: preliminary; translated from GB/EMBL/DDDBJ
 A;Molecule type: mRNA
 A;Residues: 1-690 <KVI>
 A;Cross-references: EMBL:L20313; NID:G431609; PIDN:AAA18838.1; PID:G431610
 A;Experimental source: liver
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: iron binding

Query Match
 Best Local Similarity 91.4%; Score 32; DB 2; Length 690;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 Db 186 CKGDC 190
 |||||

RESULT 11
 C87789
 protein C34G6.6 [imported] - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C;Accession: C87789
 R;anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
 A;Reference number: A75000; MUID:99069613; PMID:9851916
 A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.eleg
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A;Accession: C87789
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1011 <STO>
 A;Cross-references: GB:chr_I; PIDN:AAB52479.1; PID:g1943841; GSPDB:GN00019; CESP:C34G6.6
 C;Genetics:
 A;Gene: C34G6.6
 A;Map position: 1

Query Match
 Best Local Similarity 91.4%; Score 32; DB 2; Length 1011;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 Db 879 CKGDC 883
 |||||

Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
|:|:|
Db 301 CRGDC 305

RESULT 3

T26044

hypothetical protein W01C8.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T26044

R:Nhan, M.

submitted to The EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid W01C8.

A:Reference number: Z20142

A:Accession: T26044

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1076 <NHA>

A:Cross-references: EMBL:U41508; PIDN:AAA82623.1; CESP:W01C8.3

A:Gene: CESP:W01C8.3

A:Introns: 59/3; 92/2; 157/3; 189/3; 220/2; 251/3; 275/2; 319/1; 374/3; 407/2

Query Match

Best Local Similarity 100.0%; Score 35; DB 2; Length 1076;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5

|:|:|

Db 278 CRGDC 282

RESULT 4

B45206

metallothionein 2 - Caenorhabditis elegans

N:Alternate names: metallothionein I

C:Species: Caenorhabditis elegans

C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 29-Oct-1999

C:Accession: B45206; S09714; T29721

R:Freedman, J.H.; Slice, L.W.; Dixon, D.; Fire, A.; Rubin, C.S.

J. Biol. Chem. 268, 2554-2564, 1993

A:Title: The novel metallothionein genes of Caenorhabditis elegans. Structural organization

A:Reference number: A45206; MUID:93155063; PMID:8428932

A:Accession: B45206

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-75 <FRE>

A:Note: sequence extracted from NCBI backbone (NCBIP:124147)

R:Imagawa, M.; Onozawa, T.; Okumura, K.; Oeada, S.; Nishihara, T.; Kondo, M.

Biochem. J. 268, 237-240, 1990

A:Title: Characterization of metallothionein cDNAs induced by cadmium in the nematode Ca

A:Reference number: S09714; MUID:90262552; PMID:2344361

A:Accession: S09714

A:Molecule type: mRNA

A:Residues: 1-75 <IMA>

A:Cross-references: EMBL:X53244; NID:g6779; PIDN:CAA37334.1; PID:g6780

R:Greco, T.; Bradshaw, H.

submitted to The EMBL Data Library, July 1996

A:Description: The sequence of C. elegans cosmid K11G9.

A:Reference number: Z20672

A:Accession: T29721

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-75 <GRE>

A:Cross-references: EMBL:U64853; PIDN:AAB04979.1; GSPDB:GN00023; CESP:K11G9.6

A:Experimental source: strain Bristol N2; clone K11G9

C:Genetics:

A:Gene: CESP:K11G9.6

A:Map position: 5

A:Introns: 6/1
C:Superfamily: metallothionein

Query Match 91.4%; Score 32; DB 2; Length 75;
Best Local Similarity 80.0%; Pred. No. 26;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5

|:|:|

Db 44 CRGDC 48

RESULT 5

T48370

hypothetical protein F12E4.220 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 28-Jul-2000

C:Accession: T48370

R:Devan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.;

submitted to the Protein Sequence Database, March 2000

A:Reference number: Z24492

A:Accession: T48370

A:Molecule type: DNA

A:Residues: 1-132 <BEV>

A:Cross-references: EMBL:AL162751

A:Experimental source: cultivar Columbia; BAC clone F12E4

C:Genetics:

A:Map position: 5

A:Introns: 30/2; 76/3

A:Note: F12E4.220

C:Superfamily: Arabidopsis thaliana hypothetical protein F12E4.220

Query Match

Best Local Similarity 91.4%; Score 32; DB 2; Length 132;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5

|:|:|

Db 127 CRGDC 131

RESULT 6

A48608

E1 glycoprotein - eastern equine encephalomyelitis virus (fragment)

C:Species: eastern equine encephalomyelitis virus

C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999

C:Accession: A48608

R:Weaver, S.C.; Bellev, L.A.; Gousset, L.; Repik, P.M.; Scott, T.W.; Holland, J.J.

Virology 195, 700-709, 1993

A:Title: Diversity within natural populations of eastern equine encephalomyelitis virus.

A:Reference number: A48608; MUID:93331728; PMID:8101674

A:Contents: 215-85, MD85B

A:Accession: A48608

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-207 <WEA>

A:Cross-references: GB:S63996; NID:G400551; PIDN:AAB27576.1; PID:G400552

A:Note: sequence extracted from NCBI backbone (NCBIN:135481, NCBIP:135482)

C:Superfamily: togavirus structural polyprotein

C:Keywords: glycoprotein

Query Match

Best Local Similarity 91.4%; Score 32; DB 2; Length 207;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5

|:|:|

Db 143 CRGDC 147

RESULT 7

D85098

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2004, 06:46:27 ; Search time 39 Seconds
(without alignments)
12.332 Million cell updates/sec

Title: US-09-912-609-9

Perfect score: 35

Sequence: 1 CRGDC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	350	2 T25451	transforming growth
2	35	100.0	373	2 PW0042	activin - fruit fly
3	35	100.0	1076	2 T26044	hypothetical prote
4	32	91.4	75	2 B45206	metallothionein 2
5	32	91.4	132	2 T48370	hypothetical prote
6	32	91.4	207	2 A48608	E1 glycoprotein -
7	32	91.4	210	2 D85098	hypothetical prote
8	32	91.4	441	2 S45284	growth/differentia
9	32	91.4	654	2 S53805	beta-glucosidase/x
10	32	91.4	690	2 T11749	transferrin - Atla
11	32	91.4	1011	2 C87789	protein C34G6.6 [i
12	32	91.4	1239	1 VHWVEE	structural polypro
13	32	91.4	1240	1 VHWVEE	genome polyprotein
14	32	91.4	1241	2 S26373	structural polypro
15	32	91.4	1242	2 S72350	structural polypro
16	32	91.4	1242	2 A56605	structural polypro
17	32	91.4	1254	1 VHWVVE	structural polypro
18	32	91.4	1254	1 VHWVVE	structural polypro
19	32	91.4	1254	1 JQ1978	structural polypro
20	32	91.4	1254	1 JQ1978	structural polypro
21	32	91.4	1255	1 B44213	structural polypro
22	32	91.4	1255	1 D44213	structural polypro
23	32	91.4	2090	2 T30075	hypothetical prote
24	32	91.4	2153	2 T30074	hypothetical prote
25	31	88.6	80	2 E83128	hypothetical prote
26	31	88.6	154	2 A96544	hypothetical prote
27	31	88.6	247	2 F71545	probable oligopept
28	31	88.6	249	1 S47153	type IV prelinin p
29	31	88.6	342	2 H86300	F19K19.12 protein

30 31 88.6 442 2 S50062 cell wall glycopro
31 31 88.6 630 2 A12893 hypothetical prote
32 31 88.6 630 2 D97669 hypothetical prote
33 31 88.6 828 1 T00534 S-receptor kinase
34 30 85.7 95 2 F72864 AcOrf-117 protein
35 30 85.7 95 2 T41855 AcNPNV orf117 - Bo
36 30 85.7 102 2 A36192 inhibit beta-A cha
37 30 85.7 102 2 S36492 E7 protein - human
38 30 85.7 102 2 S36486 E7 protein - human
39 30 85.7 103 1 W7WL8 E7 protein - human
40 30 85.7 103 1 W7WL47 E7 protein - human
41 30 85.7 103 1 W7WL5 E7 protein - human
42 30 85.7 103 1 W7WLBS E7 protein - human
43 30 85.7 103 2 S16539 E7 protein - human
44 30 85.7 115 2 PN0504 activin beta A cha
45 30 85.7 124 2 C96559 F5F19.3 [imported]

ALIGNMENTS

RESULT 1

T25451

transforming growth factor beta homolog - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000

C;Accession: T25451

R;Bentley, D.

submitted to the EMBL Data Library, December 1996

A;Description: The sequence of C. elegans cosmid B0412.

A;Reference number: Z20037

A;Accession: T25451

A;Status: preliminary; translated from GB/EMBL/DDBB

A;Molecule type: DNA

A;Residues: 1-350 <BEN>

A;Cross-references: EMBL:U0953; PIDN:AAB52554.1; GSPDB:GN00021

A;Experimental source: strain Bristol N2; clone B0412

C;Genetics:

A;Gene: daf-7

A;Map position: 3

A;Introns: 43/3; 123/3; 184/2; 288/3

C;Superfamily: inhibin

Query Match 100.0%; Score 35; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 278 CRGDC 282

RESULT 2

PW0042

activin - fruit fly (Drosophila sp.) (fragment)

C;Species: Drosophila sp.

C;Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 17-Nov-2000

C;Accession: PW0042

R;Kutty, G.; Kutty, R.K.; Samuel, W.; Duncan, T.; Jaworski, C.; Wiggert, B.

Biochem. Biophys. Res. Commun. 246, 644-649, 1998

A;Title: Identification of a new member of transforming growth factor-beta superfamily ir

A;Reference number: PW0042; MUID:98289585; PMID:9618266

A;Accession: PW0042

A;Molecule type: mRNA

A;Residues: 1-373 <KUT>

A;Cross-references: GB:AF054822

C;Genetics:

A;Cross-references: FlyBase:FBgn0024913

A;Start codon: GGT

A;Introns: 86/3

C;Superfamily: inhibin

Query Match 100.0%; Score 35; DB 2; Length 373;

US-08-335-832-41

Query Match 74.3%; Score 26; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RGDC 5
Db 1 RGDC 4

RESULT 14

US-08-753-781-34
; Sequence 34, Application US/08753781C
; Patent No. 5951981
; GENERAL INFORMATION:
; APPLICANT: Markland Jr., Francis S.
; APPLICANT: Bush, Larry R.
; APPLICANT: Swenson, Stephen
; APPLICANT: Flores Sanchez, Eladio
; TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
; FILE REFERENCE: DITI 124
; CURRENT APPLICATION NUMBER: US/08/753,781C
; CURRENT FILING DATE: 1996-12-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 4

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)
OTHER INFORMATION: AMIDATION
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:synthetic
OTHER INFORMATION: peptide
US-08-753-781-34

Query Match 74.3%; Score 26; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RGDC 5
Db 1 RGDC 4

RESULT 15

US-09-141-127-14
; Sequence 14, Application US/09141127A
; Patent No. 6083481
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: THROMBUS IMAGING AGENTS
; FILE REFERENCE: DITI 113.1USC1
; CURRENT APPLICATION NUMBER: US/09/141,127A
; CURRENT FILING DATE: 1998-08-27
; EARLIER APPLICATION NUMBER: 08/335,832
; EARLIER FILING DATE: 1995-01-05
; EARLIER APPLICATION NUMBER: PCT/US93/04794
; EARLIER FILING DATE: 1993-05-21
; EARLIER APPLICATION NUMBER: 07/886,752
; EARLIER FILING DATE: 1992-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 4

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; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Modified-site
; OTHER INFORMATION: /note= "Cys is Ac-Cys."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= Modified-site
; OTHER INFORMATION: /note= "Asp is Asp-penicillamine"
US-08-240-711-4
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Query Match 74.3%; Score 26; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CRGD 4
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Db 1 CRGD 4
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RESULT 12
US-08-457-753-4
; Sequence 4, Application US/08457753
; Patent No. 5759512
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: MATHEWS, ANTHONY J.
; TITLE OF INVENTION: HEMOGLOBINS AS DRUG DELIVERY AGENTS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,753
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/240,711
; FILING DATE: 12-JUL-1994
; APPLICATION NUMBER: PCT/US92/09713
; FILING DATE: 06-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,177
; FILING DATE: 08-NOV-1991
; APPLICATION NUMBER: US 07/789,179
; FILING DATE: 08-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: ANDERSON=5A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Modified-site
; OTHER INFORMATION: /note= "Cys is Ac-Cys."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= Modified-site
; OTHER INFORMATION: /note= "Asp is Asp-penicillamine"
US-08-457-753-4

Query Match 74.3%; Score 26; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGD 4
    ||||
Db 1 CRGD 4

RESULT 13
US-08-335-832-41
; Sequence 41, Application US/08335832
; Patent No. 5925331
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Thrombus Imaging
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,832
; FILING DATE: 05-JAN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5925331nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,216-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetyl
; OTHER INFORMATION: /note= "The amino terminus is modified by covalent
; OTHER INFORMATION: linkage to an acetyl group."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= Amide
; OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
; OTHER INFORMATION: amide"
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,002
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/625,695
FILING DATE: 03-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,186
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 2748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-924-002-10

Query Match 100.0%; Score 35; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 9
5318899-77
Patent No. 5318899
APPLICANT: SCARBOROUGH, ROBERT M.; WOLF, DAVID L.; CHARO,
ISRAEL F.
TITLE OF INVENTION: PLATELET AGGREGATION INHIBITORS
NUMBER OF SEQUENCES: 83
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/483,229
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 418,028
FILING DATE: 06-OCT-1989
APPLICATION NUMBER: 367,509
FILING DATE: 16-JUN-1989
SEQ ID NO: 77:
LENGTH: 5
5318899-77

Query Match 91.4%; Score 32; DB 6; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 10
US-09-660-377A-11
Sequence 11, Application US/09660377A
Patent No. 6685914
GENERAL INFORMATION:
APPLICANT: Liu, Shuang
TITLE OF INVENTION: Macrocyclic Chelants For Metallopharmaceuticals
FILE REFERENCE: BMS-2207
CURRENT APPLICATION NUMBER: US/09/660,377A
CURRENT FILING DATE: 2000-09-12

PRIOR APPLICATION NUMBER: 60/153,512
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patent In Release #1.0, Version #1.25
SEQ ID NO 11
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(5)
OTHER INFORMATION: Cyclo
US-09-660-377A-11

Query Match 85.7%; Score 30; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 11
US-08-240-711-4
Sequence 4, Application US/08240711
Patent No. 5679777
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTHONY J.
TITLE OF INVENTION: HEMOGLOBINS AS DRUG DELIVERY AGENTS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,711
FILING DATE: 12-JUL-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09713
FILING DATE: 06-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,177
FILING DATE: 08-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,179
FILING DATE: 08-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON=5A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 5
US-08-753-781-35
; Sequence 35, Application US/08753781C
; Patent No. 5951981
; GENERAL INFORMATION:
; APPLICANT: Markland Jr., Francis S.
; APPLICANT: Bush, Larry R.
; APPLICANT: Swenson, Stephen
; APPLICANT: Flores Sanchez, Eladio
; TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
; FILE REFERENCE: DITI 124
; CURRENT APPLICATION NUMBER: US/08/753,781C
; CURRENT FILING DATE: 1996-12-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-08-753-781-35

Query Match 100.0%; Score 35; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 6
US-08-286-861-37
; Sequence 37, Application US/08286861
; Patent No. 5981478
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: No. 5981478e1 Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286.861
; FILING DATE: 04-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 7
US-09-141-127-15
; Sequence 15, Application US/09141127A
; Patent No. 6083481
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: THROMBUS IMAGING AGENTS
; FILE REFERENCE: DITI 113.IUSC1
; CURRENT APPLICATION NUMBER: US/09/141,127A
; CURRENT FILING DATE: 1998-08-27
; EARLIER APPLICATION NUMBER: 08/335,832
; EARLIER FILING DATE: 1995-01-05
; EARLIER APPLICATION NUMBER: PCT/US93/04794
; EARLIER FILING DATE: 1993-05-21
; EARLIER APPLICATION NUMBER: 07/886,752
; EARLIER FILING DATE: 1992-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-09-141-127-15

Query Match 100.0%; Score 35; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 8
US-08-924-002-10
; Sequence 10, Application US/08924002
; Patent No. 6177542
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki I.
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

; Sequence 8, Application US/08425238
; Patent No. 5627263
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/425,238
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9775
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-425-238-8

Query Match 100.0%; Score 35; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 3
US-08-625-695A-10
; Sequence 10, Application US/08625695A
; Patent No. 5912234
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki I.
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,695A

; FILING DATE: 03-APR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,186
; FILING DATE: 11-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 2041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; US-08-625-695A-10

Query Match 100.0%; Score 35; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 4
US-08-335-832-42
; Sequence 42, Application US/08335832
; Patent No. 5925331
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Thrombus Imaging
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,832
; FILING DATE: 05-JAN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5925331man, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,216-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-335-832-42

Query Match 100.0%; Score 35; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: September 22, 2004, 07:06:24 ; Search time 17 Seconds
(without alignments)
15.184 Million cell updates/sec

Title: US-09-912-609-9
Perfect score: 35
Sequence: 1 CRGDC 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 24558

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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4: /cgn2_6/prodata/2/iaa/6B COMB pep.*
5: /cgn2_6/prodata/2/iaa/6C COMB pep.*
6: /cgn2_6/prodata/2/iaa/6D COMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	5	1	US-08-212-186A-10
2	35	100.0	5	1	US-08-425-238-8
3	35	100.0	5	2	US-08-625-695A-10
4	35	100.0	5	2	US-08-335-832-42
5	35	100.0	5	2	US-08-753-781-35
6	35	100.0	5	2	US-08-286-861-37
7	35	100.0	5	3	US-09-141-127-15
8	35	100.0	5	3	US-08-924-002-10
9	32	91.4	5	6	5318899-77
10	30	85.7	5	4	US-09-660-377A-11
11	26	74.3	4	1	US-08-240-711-4
12	26	74.3	4	1	US-08-457-753-4
13	26	74.3	4	2	US-08-335-832-41
14	26	74.3	4	2	US-08-753-781-34
15	26	74.3	4	3	US-09-141-127-14
16	26	74.3	4	3	US-08-960-054A-1
17	26	74.3	4	4	US-08-958-993A-1
18	26	74.3	4	4	US-08-959-206A-1
19	26	74.3	4	4	US-09-925-715-4
20	26	74.3	4	6	5384309-4
21	26	74.3	5	1	US-07-885-202A-1
22	26	74.3	5	1	US-08-425-787-1
23	26	74.3	5	1	US-08-425-475-1
24	26	74.3	5	1	US-08-406-862-1
25	26	74.3	5	1	US-08-406-935-1
26	26	74.3	5	1	US-08-482-880-1
27	26	74.3	5	2	US-08-273-274-1

28 74.3 5 2 US-08-475-041-1 Sequence 1, Appli
29 74.3 5 2 US-08-484-773-1 Sequence 1, Appli
30 74.3 5 2 US-08-361-864-5 Sequence 5, Appli
31 74.3 5 2 US-08-361-864-5 Sequence 35, Appli
32 74.3 5 4 US-09-540-448-24 Sequence 24, Appli
33 74.3 5 4 US-09-243-640-22 Sequence 22, Appli
34 74.3 5 4 US-08-929-847-24 Sequence 24, Appli
35 74.3 5 5 PCT-US93-09916-1 Sequence 1, Appli
36 74.3 5 5 PCT-US93-09933-1 Sequence 1, Appli
37 74.3 5 5 PCT-US93-09963-1 Sequence 1, Appli
38 74.3 5 5 PCT-US94-01678-1 Sequence 1, Appli
39 74.3 5 6 5318899-78 Patent No. 5318899
40 74.3 5 6 5384309-2 Patent No. 5384309
41 74.3 5 6 5384309-5 Patent No. 5384309
42 74.3 5 6 5384309-6 Patent No. 5384309
43 74.3 5 6 5384309-7 Patent No. 5384309
44 74.3 5 3 US-09-163-095-3 Sequence 3, Appli
45 68.6

ALIGNMENTS

RESULT 1
US-08-212-186A-10
; Sequence 10, Application US/08212186A
; Patent No. 5536814
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki I.
; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,186A
; FILING DATE: 11-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9861
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: both
US-08-212-186A-10

Query Match 100.0%; Score 35; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 2
US-08-425-238-8

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RESULT 14
 US-10-853-895-3
 ; Sequence 3, Application US/10853895
 ; GENERAL INFORMATION:
 ; APPLICANT: Ponzoni, Mirco
 ; APPLICANT: Corti, Angelo
 ; APPLICANT: Allen, Theresa
 ; TITLE OF INVENTION: TUMOR TARGETED DRUG DELIVERY
 ; TITLE OF INVENTION: SYSTEMS AND USES THEREOF
 ; FILE REFERENCE: 11464-006-999 (108463-999004)
 ; CURRENT APPLICATION NUMBER: US/10/853,895
 ; CURRENT FILING DATE: 2004-05-26
 ; PRIOR APPLICATION NUMBER: GB 0312309.8
 ; PRIOR FILING DATE: 2003-05-29
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-853-895-3

Query Match 62.9%; Score 22; DB 6; Length 5;
 Best Local Similarity 60.0%; Pred. No. 6.5e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 Db 1 CNRC 5

RESULT 15
 US-10-287-811A-12
 ; Sequence 12, Application US/10287811A
 ; GENERAL INFORMATION:
 ; APPLICANT: Molmed Spa
 ; TITLE OF INVENTION: MODIFIED CYTOKINES FOR USE IN CANCER THERAPY
 ; FILE REFERENCE: P014717USM CLM
 ; CURRENT APPLICATION NUMBER: US/10/287,811A
 ; CURRENT FILING DATE: 2002-11-05
 ; PRIOR APPLICATION NUMBER: IT MI2000A000249
 ; PRIOR FILING DATE: 2000-02-15
 ; PRIOR APPLICATION NUMBER: C.I.P from US 10/218,906
 ; PRIOR FILING DATE: 2001-02-13
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: ligand
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (1)..(5)
 ; OTHER INFORMATION: where peptide is cyclic or linear
 US-10-287-811A-12

Query Match 62.9%; Score 22; DB 6; Length 5;
 Best Local Similarity 60.0%; Pred. No. 6.5e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 Db 1 CNRC 5

Search completed: September 22, 2004, 07:19:49
 Job time : 64 secs

US-10-714-564A-259
 ; Sequence 259, Application US/10714564A
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; APPLICANT: Michaud, Stephanie D.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
 ; TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
 ; FILE REFERENCE: 100086.418
 ; CURRENT APPLICATION NUMBER: US/10/714,564A
 ; CURRENT FILING DATE: 2003-11-14
 ; NUMBER OF SEQ ID NOS: 1402
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 259
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Exemplary cyclic peptide
 US-10-714-564A-259

Query Match 71.4%; Score 25; DB 6; Length 5;
 Best Local Similarity 80.0%; Pred. No. 6.5e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGDC 5
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 Db 1 CRGWC 5

RESULT 11

US-10-785-924-3
 ; Sequence 3, Application US/10785924
 ; GENERAL INFORMATION:
 ; APPLICANT: Gilchrist, Barbara A.
 ; APPLICANT: Yaar, Mina
 ; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE
 ; FILE REFERENCE: 0054.1092-012
 ; CURRENT APPLICATION NUMBER: US/10/785,924
 ; CURRENT FILING DATE: 2004-02-24
 ; PRIOR APPLICATION NUMBER: US 09/866,898
 ; PRIOR FILING DATE: 2001-05-29
 ; PRIOR APPLICATION NUMBER: US 09/163,095
 ; PRIOR FILING DATE: 1998-09-29
 ; PRIOR APPLICATION NUMBER: PCT/US97/04966
 ; PRIOR FILING DATE: 1997-03-28
 ; PRIOR APPLICATION NUMBER: US 08/625,765
 ; PRIOR FILING DATE: 1996-03-29
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Cyclic peptide
 US-10-785-924-3

Query Match 68.6%; Score 24; DB 6; Length 5;
 Best Local Similarity 60.0%; Pred. No. 6.5e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGDC 5
 ||||
 Db 1 CRGAC 5

RESULT 12

PCT-US04-29095-2
 ; Sequence 2, Application PC/TUS0429095
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of Colorado
 ; APPLICANT: Koch, Tad

; APPLICANT: Coleman, Michael P.
 ; APPLICANT: Cogan, Peter S.
 ; APPLICANT: Burke, Patrick J.
 ; APPLICANT: Post, Glen C.
 ; APPLICANT: Burkhardt, David J.
 ; APPLICANT: McKenzie, Andrew L.
 ; APPLICANT: Jackson, Katrina L.
 ; APPLICANT: Kalet, Brian T.
 ; TITLE OF INVENTION: Targeted Drug-Formaldehyde Conjugates and Methods of Making and Use
 ; TITLE OF INVENTION: Same
 ; FILE REFERENCE: 2848-59-PCT
 ; CURRENT APPLICATION NUMBER: PCT/US04/29095
 ; CURRENT FILING DATE: 2004-09-14
 ; PRIOR APPLICATION NUMBER: 60/500,508
 ; PRIOR FILING DATE: 2003-09-05
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: tumor homing peptide
 PCT-US04-29095-2

Query Match 62.9%; Score 22; DB 1; Length 5;
 Best Local Similarity 60.0%; Pred. No. 6.5e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRGDC 5
 ||||
 Db 1 CNGRC 5

RESULT 13

US-10-839-037-37
 ; Sequence 37, Application US/10839037
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/10/839,037
 ; CURRENT FILING DATE: 2004-05-04
 ; PRIOR APPLICATION NUMBER: US/09/843,221A
 ; PRIOR FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 37
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: modified bovine PTH
 US-10-839-037-37

Query Match 62.9%; Score 22; DB 6; Length 5;
 Best Local Similarity 60.0%; Pred. No. 6.5e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRGDC 5
 ||||
 Db 1 CNGRC 5

Db 1 RGDC 4

RESULT 6
US-10-111-983-4826
; Sequence 4826, Application US/10111983
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: GALEOTTI Cesira
; APPLICANT: GRANDI Guido
; APPLICANT: MASIGNANI Vega
; APPLICANT: MORA Mariarosa
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: RAPPUOLI Rino
; APPLICANT: RATTI Giulio
; APPLICANT: SCARLATO Vincenzo
; APPLICANT: SCARSELLI Maria
; TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES
; FILE REFERENCE: 2300-1654 (PP01654.003)
; CURRENT APPLICATION NUMBER: US/10/111,983
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US-60/162616
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 37764
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 4826
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Neisseria
US-10-111-983-4826

Query Match 74.3%; Score 26; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RGDC 5
Db 2 RGDC 5

RESULT 7
US-10-111-983-18704
; Sequence 18704, Application US/10111983
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: GALEOTTI Cesira
; APPLICANT: GRANDI Guido
; APPLICANT: MASIGNANI Vega
; APPLICANT: MORA Mariarosa
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: RAPPUOLI Rino
; APPLICANT: RATTI Giulio
; APPLICANT: SCARLATO Vincenzo
; APPLICANT: SCARSELLI Maria
; TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES
; FILE REFERENCE: 2300-1654 (PP01654.003)
; CURRENT APPLICATION NUMBER: US/10/111,983
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US-60/162616
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 37764
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 18704
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Neisseria
US-10-111-983-18704

Query Match 74.3%; Score 26; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RGDC 5

Db 2 RGDC 5

RESULT 8
US-10-111-983-30763
; Sequence 30763, Application US/10111983
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: GALEOTTI Cesira
; APPLICANT: GRANDI Guido
; APPLICANT: MASIGNANI Vega
; APPLICANT: MORA Mariarosa
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: RAPPUOLI Rino
; APPLICANT: RATTI Giulio
; APPLICANT: SCARLATO Vincenzo
; APPLICANT: SCARSELLI Maria
; TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES
; FILE REFERENCE: 2300-1654 (PP01654.003)
; CURRENT APPLICATION NUMBER: US/10/111,983
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US-60/162616
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 37764
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 30763
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Neisseria
US-10-111-983-30763

Query Match 74.3%; Score 26; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RGDC 5
Db 2 RGDC 5

RESULT 9
US-10-869-355-8
; Sequence 8, Application US/10869355
; GENERAL INFORMATION:
; APPLICANT: Zhang, Dongxiao
; TITLE OF INVENTION: METHODS OF SCREENING FOR MONOCLONAL
; FILE REFERENCE: EPIT-007
; CURRENT APPLICATION NUMBER: US/10/869,355
; CURRENT FILING DATE: 2004-06-15
; PRIOR APPLICATION NUMBER: 60/483,391
; PRIOR FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 60/484,185
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-869-355-8

Query Match 74.3%; Score 26; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RGDC 5
Db 2 RGDC 5

RESULT 10

;/ TITLE OF INVENTION: METHODS
;/ FILE REFERENCE: TSRI-987.LPC
;/ CURRENT APPLICATION NUMBER: PCT/US04/13212
;/ CURRENT FILING DATE: 2004-05-05
;/ PRIOR APPLICATION NUMBER: 60/467,188
;/ PRIOR FILING DATE: 2003-05-01
;/ NUMBER OF SEQ ID NOS: 20
;/ SOFTWARE: FastSeq for Windows Version 4.0
;/ SEQ ID NO 13
;/ LENGTH: 5
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: CYCLIC CADHERIN ANTAGONIST, DISULFIDE BOND BETWEEN
;/ OTHER INFORMATION: Cys1 and Cys5
PCT-US04-13212-13

Query Match 82.9%; Score 29; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGDC 5
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DB 1 CRADC 5

RESULT 3

US-10-836-289-13
;/ Sequence 13, Application US/10836289
;/ GENERAL INFORMATION:
;/ APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
;/ APPLICANT: FRIEDLANDER, Martin
;/ APPLICANT: DORRELL, Michael. I.
;/ TITLE OF INVENTION: SELECTIVE R-CADHERIN ANTAGONISTS AND
;/ TITLE OF INVENTION: METHODS
;/ FILE REFERENCE: TSRI-987.1
;/ CURRENT APPLICATION NUMBER: US/10/836,289
;/ CURRENT FILING DATE: 2004-04-30
;/ PRIOR APPLICATION NUMBER: 60/467,188
;/ PRIOR FILING DATE: 2003-05-01
;/ NUMBER OF SEQ ID NOS: 20
;/ SOFTWARE: FastSeq for Windows Version 4.0
;/ SEQ ID NO 13
;/ LENGTH: 5
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: CYCLIC CADHERIN ANTAGONIST, DISULFIDE BOND BETWEEN
;/ OTHER INFORMATION: Cys1 and Cys5
US-10-836-289-13

Query Match 82.9%; Score 29; DB 6; Length 5;
Best Local Similarity 80.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGDC 5
|||
DB 1 CRADC 5

RESULT 4

US-10-475-104-1
;/ Sequence 1, Application US/10475104
;/ GENERAL INFORMATION:
;/ APPLICANT: Schneider-Mergener, Jens
;/ APPLICANT: Schutkowski, Mike
;/ APPLICANT: Reimer, Ulf
;/ APPLICANT: Dong, Liying
;/ APPLICANT: Farnse, Soren
;/ APPLICANT: Scharn, Dirk
;/ APPLICANT: Osterkamp, Frank
;/ APPLICANT: Hummel, Gerd
;/ APPLICANT: Jobron, Laurence

;/ TITLE OF INVENTION: Method for Determining the Substrate Specificity of an Enzymatic
;/ FILE REFERENCE: 2918-0102
;/ CURRENT APPLICATION NUMBER: US/10/475,104
;/ CURRENT FILING DATE: 2003-10-17
;/ PRIOR APPLICATION NUMBER: PCT/EP02/04265
;/ PRIOR FILING DATE: 2002-04-17
;/ NUMBER OF SEQ ID NOS: 144
;/ SOFTWARE: PatentIn version 3.2
;/ SEQ ID NO 1
;/ LENGTH: 4
;/ TYPE: PRT
;/ ORGANISM: Unknown
;/ FEATURE:
;/ OTHER INFORMATION: cell-adhesive peptide
US-10-475-104-1

Query Match 74.3%; Score 26; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RGDC 5
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DB 1 RGDC 4

RESULT 5

US-10-734-730-4
;/ Sequence 4, Application US/10734730
;/ GENERAL INFORMATION:
;/ APPLICANT: Klaveness, Jo
;/ APPLICANT: Rongved, Pal
;/ APPLICANT: Hogset, Anders
;/ APPLICANT: Tollshaug, Helge
;/ APPLICANT: Cuthbertson, Alan
;/ APPLICANT: Godal, Aslak
;/ APPLICANT: Hoff, Lars
;/ APPLICANT: Gogstad, Geir
;/ APPLICANT: Bryn, Klaus
;/ APPLICANT: Naevestad, Anne
;/ APPLICANT: Lovhaug, Dagfinn
;/ APPLICANT: Hellebust, Halldis
;/ APPLICANT: Solbakken, Magne
;/ TITLE OF INVENTION: Diagnostic/Therapeutic Agents
;/ FILE REFERENCE: NIDN-10314
;/ CURRENT APPLICATION NUMBER: US/10/734,730
;/ CURRENT FILING DATE: 2003-12-15
;/ PRIOR APPLICATION NUMBER: 09/925,715
;/ PRIOR FILING DATE: 2001-08-10
;/ PRIOR APPLICATION NUMBER: 08/959,206
;/ PRIOR FILING DATE: 1997-10-28
;/ PRIOR APPLICATION NUMBER: 60/049,263
;/ PRIOR FILING DATE: 1997-06-07
;/ PRIOR APPLICATION NUMBER: 60/049,264
;/ PRIOR FILING DATE: 1997-08-06
;/ PRIOR APPLICATION NUMBER: 60/049,266
;/ PRIOR FILING DATE: 1997-06-07
;/ NUMBER OF SEQ ID NOS: 20
;/ SOFTWARE: PatentIn version 3.1
;/ SEQ ID NO 4
;/ LENGTH: 4
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic RGDC sequence
US-10-734-730-4

Query Match 74.3%; Score 26; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RGDC 5
|||

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OM protein - protein search, using sw model

Run on: September 22, 2004, 07:08:54 ; Search time 62 Seconds
(without alignments)
10.974 Million cell updates/sec

Title: US-09-912-609-9

Perfect score: 35

Sequence: 1 CRGDC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 735861 seqs, 136079791 residues

Total number of hits satisfying chosen parameters: 17204

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Pending Patents AA New.*
- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
 - 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	30	85.7	5	6	US-10-342-081-77	Sequence 77, Appl
2	29	82.9	5	1	PCT-US04-13212-13	Sequence 13, Appl
3	29	82.9	5	6	US-10-836-289-13	Sequence 13, Appl
4	26	74.3	4	6	US-10-475-104-1	Sequence 1, Appl
5	26	74.3	4	6	US-10-734-730-4	Sequence 4, Appl
6	26	74.3	5	6	US-10-111-983-4826	Sequence 4826, Ap
7	26	74.3	5	6	US-10-111-983-18704	Sequence 18704, A
8	26	74.3	5	6	US-10-111-983-30763	Sequence 30763, A
9	26	74.3	5	6	US-10-869-355-8	Sequence 8, Appl
10	25	71.4	5	6	US-10-714-564A-259	Sequence 259, App
11	24	68.6	5	6	US-10-785-924-3	Sequence 3, Appl
12	22	62.9	5	1	PCT-US04-29095-2	Sequence 2, Appl
13	22	62.9	5	6	US-10-839-037-37	Sequence 37, Appl
14	22	62.9	5	6	US-10-853-895-3	Sequence 3, Appl
15	22	62.9	5	6	US-10-287-811A-12	Sequence 12, Appl
16	22	62.9	5	6	US-10-900-339-24	Sequence 24, Appl
17	22	62.9	5	6	US-10-912-764-37	Sequence 37, Appl
18	22	62.9	5	6	US-10-712-298-24	Sequence 24, Appl
19	22	62.9	5	6	US-10-627-649-223	Sequence 223, App
20	21	60.0	4	6	US-10-815-514-41	Sequence 41, Appl
21	21	60.0	4	6	US-10-877-930-41	Sequence 41, Appl
22	21	60.0	5	6	US-10-111-983-7653	Sequence 7653, Ap
23	21	60.0	5	6	US-10-111-983-20982	Sequence 20982, A
24	21	60.0	5	6	US-10-111-983-33204	Sequence 33204, A
25	21	60.0	5	6	US-10-712-425-384	Sequence 384, App
26	20	57.1	5	6	US-10-665-668A-3	Sequence 3, Appl

27	20	57.1	5	6	US-10-870-765-3	Sequence 3, Appl
28	20	57.1	5	6	US-10-839-434-1	Sequence 1, Appl
29	19	54.3	4	6	US-10-853-665-17	Sequence 17, Appl
30	19	54.3	5	6	US-10-714-564A-303	Sequence 303, App
31	19	54.3	5	6	US-10-714-564A-353	Sequence 353, App
32	19	54.3	5	6	US-10-714-564A-1017	Sequence 1017, Ap
33	18	51.4	5	6	US-10-111-983-27465	Sequence 27465, A
34	18	51.4	5	6	US-10-714-564A-281	Sequence 281, App
35	18	51.4	5	6	US-10-759-379-209	Sequence 209, App
36	18	51.4	5	6	US-10-759-507-309	Sequence 209, App
37	17	48.6	3	1	PCT-US04-07269-5	Sequence 5, Appl
38	17	48.6	3	1	PCT-US04-07269-6	Sequence 6, Appl
39	17	48.6	3	1	PCT-US04-16828-1	Sequence 1, Appl
40	17	48.6	3	5	US-09-446-274A-4	Sequence 4, Appl
41	17	48.6	3	5	US-09-446-274B-4	Sequence 4, Appl
42	17	48.6	3	6	US-10-662-261A-1	Sequence 1, Appl
43	17	48.6	3	6	US-10-797-606-1	Sequence 1, Appl
44	17	48.6	3	6	US-10-059-506-7	Sequence 7, Appl
45	17	48.6	3	6	US-10-481-006-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-342-081-77
; Sequence 77, Application US/10342081
; GENERAL INFORMATION:
; APPLICANT: Rajopadhye, Milind
; APPLICANT: Edwards, D. Scott
; APPLICANT: Barrett, John A.
; APPLICANT: Carpenter, Jr., Alan P.
; APPLICANT: Harris, Thomas D.
; APPLICANT: Hemmway, Stuart J.
; APPLICANT: Liu, Shuang
; APPLICANT: Singh, Prahlad R.
; TITLE OF INVENTION: PHARMACEUTICALS FOR THE IMAGING OF ANGIOGENIC DISORDERS
; FILE REFERENCE: BMS-2024
; CURRENT APPLICATION NUMBER: US/10/342,081
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 09/599,295
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 77
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(5)
; OTHER INFORMATION: cyclic amino acid
US-10-342-081-77

Query Match 85.7%; Score 30; DB 6; Length 5;
Best Local Similarity 80.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRGDC 5
|
|
|
|
Db 1 CRGDC 5

RESULT 2
PCT-US04-13212-13
; Sequence 13, Application PC/TUS0413212
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: FRIEDLANDER, Martin
; APPLICANT: DORRELL, Michael I.
; TITLE OF INVENTION: SELECTIVE R-CADHERIN ANTAGONISTS AND

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; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-033-769-11

Query Match      85.7%; Score 30; DB 26; Length 5;
Best Local Similarity 80.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRGDC 5
        |   |
DB      1 CNGDC 5

RESULT 15
US-10-081-258-11
; Sequence 11, Application US/10081258
; GENERAL INFORMATION:
; APPLICANT: Liu, Shuang
; TITLE OF INVENTION: Ascorbic Acid Analogs For Metalloradiopharmaceuticals
; FILE REFERENCE: PH-7277 US (BMS-0746)
; CURRENT APPLICATION NUMBER: US/10/081,258
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/271,389
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-081-258-11

Query Match      85.7%; Score 30; DB 26; Length 5;
Best Local Similarity 80.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRGDC 5
        |   |
DB      1 CNGDC 5

Search completed: September 22, 2004, 07:18:39
Job time : 403 secs
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; Sequence 9, Application US/09912609
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: MATSUNAGA, TERRY ONICHI
; APPLICANT: RAMASWAMI, VARADARAJAN
; APPLICANT: ROMANOWSKI, MAREK J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 5030-0001.24
; CURRENT APPLICATION NUMBER: US/09/912,609
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/478,124
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-912-609-9

Query Match      100.0%; Score 35; DB 24; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDC 5
DB      1 CRGDC 5

RESULT 11
US-10-304-160-2
; Sequence 2, Application US/10304160
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J
; APPLICANT: KOVESDI, IMRE
; APPLICANT: ROELVINK, PETRUS W
; APPLICANT: EINFELD, DAVID
; APPLICANT: BROUGH, DOUGLAS E
; APPLICANT: LIZONOVA, ALENA
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TARGETING AN ADENOVIRAL VECTOR
; FILE REFERENCE: 220148
; CURRENT APPLICATION NUMBER: US/10/304,160
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: PCI/US01/17391
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 09/631,191
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 60/208451
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-304-160-2

Query Match      100.0%; Score 35; DB 29; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDC 5
DB      1 CRGDC 5

RESULT 12
US-60-208-451-2
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; Sequence 2, Application US/60208451
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J
; APPLICANT: KOVESDI, IMRE
; APPLICANT: ROELVINK, PETRUS W
; APPLICANT: EINFELD, DAVID
; APPLICANT: BROUGH, DOUGLAS E
; APPLICANT: LIZONOVA, ALENA
; TITLE OF INVENTION: ALTERNATIVELY TARGETED ADENOVIRUS
; FILE REFERENCE: 205046
; CURRENT APPLICATION NUMBER: US/60/208,451
; CURRENT FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-208-451-2

Query Match      100.0%; Score 35; DB 33; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDC 5
DB      1 CRGDC 5

RESULT 13
US-09-995-388-48
; Sequence 48, Application US/09995388
; GENERAL INFORMATION:
; APPLICANT: CARPENTER, JR., ALAN P.
; TITLE OF INVENTION: SIMULTANEOUS IMAGING OF CARDIAC PERFUSION AND A VITRONECTIN
; FILE REFERENCE: BMS-2201
; CURRENT APPLICATION NUMBER: US/09/995,388
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 60/253,324
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-995-388-48

Query Match      85.7%; Score 30; DB 25; Length 5;
Best Local Similarity 80.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRGDC 5
DB      1 CRGDC 5

RESULT 14
US-10-033-769-11
; Sequence 11, Application US/10033769
; GENERAL INFORMATION:
; APPLICANT: LIU, SHUANG
; TITLE OF INVENTION: POLYPODAL CHELANTS FOR METALLOPHARMACEUTICALS
; FILE REFERENCE: BMS-2204
; CURRENT APPLICATION NUMBER: US/10/033,769
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: US 60/260,619
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
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RESULT 7
US-09-364-597A-37
; Sequence 37, Application US/09364597A
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: Novel Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,597A
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,861
; FILING DATE: 04-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 3419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 535-9001
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-364-597A-37
Query Match 100.0%; Score 35; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDC 5
DB 1 CRGDC 5
RESULT 8
US-09-627-035-10
; Sequence 10, Application US/09627035
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki I.
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/627,035
FILING DATE: 27-Jul-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/212,186
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9861
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: both
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-627-035-10
Query Match 100.0%; Score 35; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDC 5
DB 1 CRGDC 5
RESULT 9
US-09-699-679A-24
; Sequence 24, Application US/09699679A
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; APPLICANT: Shen, Dekang
; APPLICANT: Wu, Guanli
; TITLE OF INVENTION: Novel Targeted Compositions For Diagnostics And Therapeutic Use
; FILE REFERENCE: UNGR1598
; CURRENT APPLICATION NUMBER: US/09/699,679A
; CURRENT FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/218,660
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 08/660,032
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 08/640,464
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/497,684
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-699-679A-24
Query Match 100.0%; Score 35; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDC 5
DB 1 CRGDC 5
RESULT 10
US-09-912-609-9

;; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
;; NUMBER OF SEQUENCES: 25
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Campbell and Flores
;; STREET: 4370 La Jolla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: USA
;; ZIP: 92122
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/625,695
;; FILING DATE:
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-LA 9861
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; TOPOLOGY: both
US-08-625-695-10

Query Match 100.0%; Score 35; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 5
US-08-753-781B-45
;; Sequence 45, Application US/08/753781B
;; GENERAL INFORMATION:
;; APPLICANT: Markland, Francis S
;; APPLICANT: Bush, Larry R
;; APPLICANT: Swenson, Stephen
;; APPLICANT: Sanchez, Eladio F
;; TITLE OF INVENTION: Thrombolytic Agents with Antithrombotic
;; TITLE OF INVENTION: Properties
;; NUMBER OF SEQUENCES: 54
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
;; STREET: 300 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/753.781B
;; FILING DATE: 02-DEC-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Noonan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 96,2056
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 312 913 0001
;; TELEFAX: 312 913 0002
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 45:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-753-781B-45

Query Match 100.0%; Score 35; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 6
US-08-982-981-45
;; Sequence 45, Application US/08982981
;; GENERAL INFORMATION:
;; APPLICANT: Markland Jr., Francis S.
;; APPLICANT: Bush, Larry R.
;; APPLICANT: Swenson, Stephen
;; APPLICANT: Flores Sanchez, Eladio
;; TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC
;; TITLE OF INVENTION: ACTIVITY
;; NUMBER OF SEQUENCES: 54
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Diatide, Inc.
;; STREET: 9 Delta Drive
;; CITY: Londonderry
;; STATE: NH
;; COUNTRY: USA
;; ZIP: 03053
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/982,981
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/753,781
;; FILING DATE: 02-DEC-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McDaniels, Patricia A.
;; REGISTRATION NUMBER: 33,194
;; REFERENCE/DOCKET NUMBER: DITI 124.1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 603 437 8970
;; TELEFAX: 603 437 8977
;; INFORMATION FOR SEQ ID NO: 45:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-982-981-45

Query Match 100.0%; Score 35; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/159,001
;; FILING DATE: 24-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hook, Gregory
;; REGISTRATION NUMBER: 38,701
;; REFERENCE/DOCKET NUMBER: FP-LA 1220
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 37:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; TOPOLOGY: circular
PCT-US94-13542-37

Query Match 100.0%; Score 35; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 2

US-07-961-889-55
; Sequence 55, Application US/07961889
; GENERAL INFORMATION:
; APPLICANT: Lobl, Thomas J.
; APPLICANT: Chiang, Shiu-Lan
; APPLICANT: Cardarelli, Pina M.
; TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Fifth Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/961,889
; FILING DATE: 04-JUN-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/550,330
; FILING DATE: 09-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Bostich, June M.
; REGISTRATION NUMBER: 31,238
; REFERENCE/DOCKET NUMBER: Tanabe #7126/PD1381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 1..5
US-07-961-889-55

Query Match 100.0%; Score 35; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 3

US-08-575-461-55
; Sequence 55, Application US/08575461
; GENERAL INFORMATION:
; APPLICANT: Lobl, Thomas J.
; APPLICANT: Chiang, Shiu-Lan
; APPLICANT: Cardarelli, Pina M.
; TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Fifth Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,461
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/961,889
; FILING DATE: 04-JUN-1993
; APPLICATION NUMBER: US 07/550,330
; FILING DATE: 09-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Bostich, June M.
; REGISTRATION NUMBER: 31,238
; REFERENCE/DOCKET NUMBER: Tanabe #7126/PD1381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 1..5
US-08-575-461-55

Query Match 100.0%; Score 35; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 4

US-08-625-695-10
; Sequence 10, Application US/08625695
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki I.
; APPLICANT: Koivunen, Erkki

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OM protein - protein search, using sw model

Run on: September 22, 2004, 07:08:29 ; Search time 402 Seconds
(without alignments)
12.140 Million cell updates/sec

Title: US-09-912-609-9

Perfect score: 35
Sequence: 1 CRGDC 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 97603577 residues

Total number of hits satisfying chosen parameters: 102010

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
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28: /cgn2_6/ptodata/2/paa/US102_COMB.pep.*
29: /cgn2_6/ptodata/2/paa/US103_COMB.pep.*
30: /cgn2_6/ptodata/2/paa/US104_COMB.pep.*
31: /cgn2_6/ptodata/2/paa/US106_COMB.pep.*
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33: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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1	35	100.0	5	1	PCT-US94-13542-37	Sequence 37, Appl
2	35	100.0	5	3	US-07-961-889-55	Sequence 55, Appl
3	35	100.0	5	9	US-08-575-461-55	Sequence 55, Appl
4	35	100.0	5	10	US-08-625-695-10	Sequence 10, Appl
5	35	100.0	5	11	US-08-753-781B-45	Sequence 45, Appl
6	35	100.0	5	13	US-08-982-981-45	Sequence 45, Appl
7	35	100.0	5	17	US-09-364-597A-37	Sequence 37, Appl
8	35	100.0	5	20	US-09-627-035-10	Sequence 10, Appl
9	35	100.0	5	20	US-09-699-679A-24	Sequence 24, Appl
10	35	100.0	5	24	US-09-912-609-9	Sequence 9, Appl
11	35	100.0	5	29	US-10-304-160-2	Sequence 2, Appl
12	35	100.0	5	33	US-60-208-451-2	Sequence 2, Appl
13	30	85.7	5	25	US-09-595-388-48	Sequence 48, Appl
14	30	85.7	5	26	US-10-033-769-11	Sequence 11, Appl
15	30	85.7	5	26	US-10-081-258-11	Sequence 11, Appl
16	30	85.7	5	31	US-10-622-246-77	Sequence 77, Appl
17	29	82.9	5	3	US-07-821-011B-23	Sequence 23, Appl
18	28	80.0	5	3	US-07-821-011B-7	Sequence 7, Appl
19	28	80.0	5	3	US-07-821-011B-12	Sequence 12, Appl
20	28	80.0	5	3	US-07-821-011B-16	Sequence 16, Appl
21	28	80.0	5	5	US-08-137-012-6	Sequence 6, Appl
22	28	80.0	5	5	US-08-137-012-10	Sequence 10, Appl
23	28	80.0	5	5	US-08-197-012-14	Sequence 14, Appl
24	28	80.0	5	5	US-08-197-012-31	Sequence 31, Appl
25	28	80.0	5	5	US-08-197-012-45	Sequence 45, Appl
26	26	74.3	4	1	PCT-US03-34909-1	Sequence 1, Appl
27	26	74.3	4	3	US-07-789-177A-4	Sequence 4, Appl
28	26	74.3	4	3	US-07-789-177B-4	Sequence 4, Appl
29	26	74.3	4	4	US-08-033-414-10	Sequence 10, Appl
30	26	74.3	4	11	US-08-753-781B-44	Sequence 44, Appl
31	26	74.3	4	13	US-08-982-981-44	Sequence 44, Appl
32	26	74.3	4	14	US-09-095-028-9	Sequence 9, Appl
33	26	74.3	4	15	US-09-122-348B-1	Sequence 1, Appl
34	26	74.3	4	20	US-09-623-548A-1125	Sequence 1125, Ap
35	26	74.3	4	20	US-09-657-276-1125	Sequence 1125, Ap
36	26	74.3	4	22	US-09-765-614B-1	Sequence 1, Appl
37	26	74.3	4	25	US-09-991-588B-1	Sequence 1, Appl
38	26	74.3	4	27	US-10-179-743A-1	Sequence 1, Appl
39	26	74.3	4	32	US-10-701-591-1	Sequence 1, Appl
40	26	74.3	4	32	US-10-722-075-1	Sequence 1, Appl
41	26	74.3	5	1	PCT-US94-13394-1	Sequence 1, Appl
42	26	74.3	5	3	US-07-692-884-6	Sequence 6, Appl
43	26	74.3	5	3	US-07-962-956-1	Sequence 1, Appl
44	26	74.3	5	3	US-07-962-956-1	Sequence 1, Appl
45	26	74.3	5	3	US-07-962-957-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
PCT-US94-13542-37
; Sequence 37, Application PC/TUS9413542
; GENERAL INFORMATION:
; APPLICANT: La Jolla Cancer Research Foundation
; TITLE OF INVENTION: Novel Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13542
; FILING DATE: 22-NOV-1994
; CLASSIFICATION:

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RESULT 14
US-09-866-898-3
; Sequence 3, Application US/09866898
; Patent No. US20020051988A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
; FILE REFERENCE: BU96-09A2
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US/09/866,898
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: PCT/US97/04966
; PRIOR FILING DATE: 1997-03-28
; PRIOR APPLICATION NUMBER: 08/625,765
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic peptide
US-09-866-898-3

Query Match 68.6%; Score 24; DB 9; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRGDC 5
|:|
Db 1 CKGAC 5

RESULT 15
US-09-018-194-3
; Sequence 3, Application US/09018194
; Publication No. US20030175231A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mina
; APPLICANT: Eller, Mark
; TITLE OF INVENTION: METHODS OF INDUCING HAIR GROWTH AND
; TITLE OF INVENTION: COLORATION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/018,194
; FILING DATE: 04-FEB-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,683
; FILING DATE: 30-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10971
; FILING DATE: 30-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/298,941

; FILING DATE: 31-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hogle, Doreen M.
; REGISTRATION NUMBER: 36,361
; REFERENCE/DOCKET NUMBER: BU94-15A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-018-194-3

Query Match 68.6%; Score 24; DB 10; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRGDC 5
|:|
Db 1 CKGAC 5

Search completed: September 22, 2004, 07:21:59
Job time : 125 secs

QY 2 RGDC 5
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Db 1 RGDC 4

RESULT 10
US-10-722-075-1
; Sequence 1, Application US/10722075
; Publication No. US20040141922A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; FILE REFERENCE: agents
; FILE REFERENCE: REF/Klaveress/054
; CURRENT APPLICATION NUMBER: US/10/722,075
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/08/960,054A
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:RGDC-Mal-PEG3400-DSPE
US-10-722-075-1

Query Match 74.3%; Score 26; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RGDC 5
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Db 1 RGDC 4

RESULT 11
US-10-475-104-1
; Sequence 1, Application US/10475104
; Publication No. US20040171097A1
; GENERAL INFORMATION:
; APPLICANT: Schneider-Mergener, Jens
; APPLICANT: Schutkowski, Mike
; APPLICANT: Reimer, Ulf
; APPLICANT: Dong, Liying
; APPLICANT: Fanse, Soren
; APPLICANT: Scharn, Dirk
; APPLICANT: Osterkamp, Frank
; APPLICANT: Hummel, Gerd
; APPLICANT: Jobron, Laurence
; TITLE OF INVENTION: Method for Determining the Substrate Specificity of an Enzymatic
; TITLE OF INVENTION: Activity and a Device Therefor
; FILE REFERENCE: 2918-0102
; CURRENT APPLICATION NUMBER: US/10/475,104
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/EP02/04265
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: cell-adhesive peptide
US-10-475-104-1

Query Match 74.3%; Score 26; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RGDC 5
|||||
Db 1 RGDC 4

RESULT 12
US-10-046-801-24
; Sequence 24, Application US/10046801
; Publication No. US20030054027A1
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/10/046,801
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/540,448
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
; OTHER INFORMATION: X is penicillamine
US-10-046-801-24

Query Match 74.3%; Score 26; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGD 4
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Db 1 CRGD 4

RESULT 13
US-10-714-564A-259
; Sequence 259, Application US/10714564A
; Publication No. US20040175361A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Michaud, Stephanie D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
; FILE REFERENCE: 100086,418
; CURRENT APPLICATION NUMBER: US/10/714,564A
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1402
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary cyclic peptide
US-10-714-564A-259

Query Match 71.4%; Score 25; DB 16; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGDC 5
|||||
Db 1 CRGWC 5

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Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGDC 5
Db 1 CNGDC 5

RESULT 6
US-09-765-614B-1
; Sequence 1, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; FILE REFERENCE: agents
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:RGDC-Mal-PEG3400-DSPE
US-09-765-614B-1

Query Match 74.3%; Score 26; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RGDC 5
Db 1 RGDC 4

RESULT 7
US-09-925-715-4
; Sequence 4, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; FILE REFERENCE: agents
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic RGDC
; OTHER INFORMATION: sequence
US-09-925-715-4

Query Match 74.3%; Score 26; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RGDC 5
Db 1 RGDC 4

RESULT 8
US-09-991-588B-1
; Sequence 1, Application US/09991588B
; Publication No. US20030219429A1
; GENERAL INFORMATION:
; APPLICANT: Budny, John A.
; TITLE OF INVENTION: Compositionand Method for Bone Regeneration
; FILE REFERENCE: 1008-120.US
; CURRENT APPLICATION NUMBER: US/09/991,588B
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 09/122,348
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Purchased commercially or sequence is synthesized
US-09-991-588B-1

Query Match 74.3%; Score 26; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RGDC 5
Db 1 RGDC 4

RESULT 9
US-10-179-743A-1
; Sequence 1, Application US/10179743A
; Publication No. US20040001959A1
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Jeffrey
; APPLICANT: Danahy, Michael P
; APPLICANT: Gwalt, Ellen S.
; APPLICANT: Schwarzbauer, Jean E.
; APPLICANT: Midwood, Kim S.
; APPLICANT: Avaltroni, Michael J.
; APPLICANT: Carolus, Michael D.
; TITLE OF INVENTION: ENHANCED BONDING LAYERS ON TITANIUM MATERIALS
; FILE REFERENCE: P22,571-1 USA
; CURRENT APPLICATION NUMBER: US/10/179,743A
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/389,574
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/300,144
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 09/668,080
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/155,398
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 08/794,833
; PRIOR FILING DATE: 1997-02-04
; PRIOR APPLICATION NUMBER: US 60/035,040
; PRIOR FILING DATE: 1997-01-13
; PRIOR APPLICATION NUMBER: US 60/028,949
; PRIOR FILING DATE: 1996-10-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: The three amino acid sequence RGD which occurs on Fibronectine ce
; OTHER INFORMATION: ll adhesion protein is modified with cystine to provide RGDC
US-10-179-743A-1

Query Match 74.3%; Score 26; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: amino acid
/ TOPOLOGY: circular
US-09-364-597A-37

Query Match      100.0%; Score 35; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDC 5
Db      1 CRGDC 5

RESULT 2
US-09-912-609-9
/ Sequence 9, Application US/09912609
/ Publication No. US20020041898A1
/ GENERAL INFORMATION:
/ APPLICANT: UNGER, EVAN C.
/ APPLICANT: MATSUNAGA, TERRY ONICHI
/ APPLICANT: RAMASWAMI, VARADARAJAN
/ APPLICANT: ROMANOWSKI, MAREK J.
/ TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
/ FILE REFERENCE: 5030-0001.24
/ CURRENT APPLICATION NUMBER: US/09/912,609
/ CURRENT FILING DATE: 2001-07-25
/ PRIOR APPLICATION NUMBER: 09/703,474
/ PRIOR FILING DATE: 2000-10-31
/ PRIOR APPLICATION NUMBER: 09/478,124
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 131
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 9
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: peptide
US-09-912-609-9

Query Match      100.0%; Score 35; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDC 5
Db      1 CRGDC 5

RESULT 3
US-10-304-160-2
/ Sequence 2, Application US/10304160
/ Publication No. US20030099619A1
/ GENERAL INFORMATION:
/ APPLICANT: WICKHAM, THOMAS J
/ APPLICANT: KOVESDI, IMRE
/ APPLICANT: ROELVINK, PETRUS W
/ APPLICANT: EINFELD, DAVID
/ APPLICANT: BROUGH, DOUGLAS E
/ APPLICANT: LIZONOVA, ALENA
/ TITLE OF INVENTION: METHOD AND COMPOSITION FOR TARGETING AN ADENO VIRAL VECTOR
/ FILE REFERENCE: 220148
/ CURRENT APPLICATION NUMBER: US/10/304,160
/ CURRENT FILING DATE: 2002-11-25
/ PRIOR APPLICATION NUMBER: PCT/US01/17391
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: US 09/631,191
/ PRIOR FILING DATE: 2000-08-09
/ PRIOR APPLICATION NUMBER: US 60/208451

PRIORITY FILING DATE: 2000-05-31
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn Ver. 3.1
/ SEQ ID NO 2
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-304-160-2

Query Match      100.0%; Score 35; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDC 5
Db      1 CRGDC 5

RESULT 4
US-09-995-388-48
/ Sequence 48, Application US/09995388
/ Publication No. US20020106325A1
/ GENERAL INFORMATION:
/ APPLICANT: Carpenter, Jr., Alan P.
/ TITLE OF INVENTION: SIMULTANEOUS IMAGING OF CARDIAC PERFUSION AND A VITRONECTIN
/ FILE REFERENCE: BMS-2201
/ CURRENT APPLICATION NUMBER: US/09/995,388
/ CURRENT FILING DATE: 2001-11-27
/ PRIOR APPLICATION NUMBER: US 60/253,324
/ PRIOR FILING DATE: 2000-11-27
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 48
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Construct
US-09-995-388-48

Query Match      85.7%; Score 30; DB 12; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRGDC 5
Db      1 CRGDC 5

RESULT 5
US-10-033-769-11
/ Sequence 11, Application US/10033769
/ Publication No. US20020094316A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Shuang
/ TITLE OF INVENTION: POLYPODAL CHELANTS FOR METALLOPHARMACEUTICALS
/ FILE REFERENCE: BMS-2204
/ CURRENT APPLICATION NUMBER: US/10/033,769
/ CURRENT FILING DATE: 2001-12-27
/ PRIOR APPLICATION NUMBER: US 60/260,619
/ PRIOR FILING DATE: 2001-01-09
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 11
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Construct
US-10-033-769-11

Query Match      85.7%; Score 30; DB 12; Length 5;
```

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	35	100.0	5	9	US-09-364-597A-37	Sequence 37, Appl
2	35	100.0	5	12	US-09-912-609-9	Sequence 9, Appl
3	35	100.0	5	14	US-10-304-160-2	Sequence 2, Appl
4	30	85.7	5	12	US-09-995-388-48	Sequence 48, Appl
5	30	85.7	5	12	US-10-033-769-11	Sequence 11, Appl
6	26	74.3	4	9	US-09-765-614B-1	Sequence 1, Appl
7	26	74.3	4	9	US-09-935-715-4	Sequence 4, Appl
8	26	74.3	4	11	US-09-991-588B-1	Sequence 1, Appl
9	26	74.3	4	13	US-10-179-743A-1	Sequence 1, Appl
10	26	74.3	4	16	US-10-722-075-1	Sequence 1, Appl
11	26	74.3	4	16	US-10-725-104-1	Sequence 1, Appl
12	26	74.3	5	14	US-10-046-801-24	Sequence 24, Appl
13	25	71.4	5	16	US-10-714-564A-259	Sequence 259, App
14	24	68.6	5	9	US-09-866-898-3	Sequence 3, Appl
15	24	68.6	5	10	US-09-018-194-3	Sequence 3, Appl

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CC The invention relates to a composition comprising a bioactive agent
CC homogeneously dispersed in a targeted matrix (polymer and targeting
CC ligand). Also included are a targeted matrix for use as a delivery
CC vehicle comprising a polymer associated with a targeting ligand,
CC enhancing the bioavailability of an agent comprising administration of
CC the composition and treating cancer comprising administration of the
CC novel composition. The method is useful for targeted delivery of a drug,
CC especially in cancer therapy. The targeting ligand may be a peptide.
CC Examples of targeting peptides are disclosed including cathepsin-D
CC substrate peptides, peptides targeting receptors in the brain and kidney,
CC peptides recognising fibronectin- and vitronectin-binding integrins,
CC peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,
CC peptides targeting the angiogenic endothelium of solid tumours, tissue
CC specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,
CC adrenal gland and retina), and cationic cancer-targeting peptides. The
CC present sequence is a peptide targeting ligand disclosed in the invention
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 35; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
| | | | |
Db 1 CRGDC 5

Search completed: September 22, 2004, 07:50:29
Job time : 122 secs

XX PF 27-AUG-1998; 98US-00141127.
 XX XX
 PR 21-MAY-1992; 92US-00886752.
 PR 21-MAY-1993; 93WO-US004794.
 PR 05-JAN-1995; 95US-00335832.
 XX XX
 PA (DIAT-) DIATIDE INC.
 XX XX
 PI Lister-James J, Dean RT;
 XX XX
 DR WPI; 2000-498061/44.
 XX XX
 XX Composition comprises technetium-99m and polyamide reagent which binds to
 PT thrombi, useful as scintigraphic imaging agent for imaging sites of
 PT thrombus formation in vivo.
 XX XX
 PS Example 2; Col 15-16; 27pp; English.
 XX XX
 CC The present sequence is that of a peptide that acts as a ligand for the
 CC GPIIb/IIIa receptor. The invention relates to radiolabeled reagents that
 CC are scintigraphic imaging agents for imaging sites of thrombus formation
 CC in vivo. The reagents each comprise a specific binding compound, such as
 CC the present peptide, that is capable of binding to at least 1 component
 CC of a thrombus, and which is covalently linked to a radiolabel-binding
 CC moiety. A method for using such a reagent labeled with technetium-99m to
 CC image a thrombus site in a mammalian body is claimed
 XX XX
 SQ Sequence 5 AA;
 - Query Match 100.0%; Score 35; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 DB |||||
 1 CRGDC 5
 RESULT 17
 AAEE17982
 ID AAEE17982 standard; peptide; 5 AA.
 XX AC AAEE17982;
 XX DT 07-MAY-2002 (first entry)
 XX DE Human ligand #2 attached to an adenoviral vector.
 XX KW Human; adenoviral coat protein; non-native ligand; cell-surface receptor;
 KW therapy; anti-tumour agent; tumour necrosis factor; cancer; brain; lung;
 KW ovary; breast; prostate.
 XX OS Homo sapiens.
 XX PN WO200192549-A2.
 XX PD 06-DEC-2001.
 XX PF 30-MAY-2001; 2001WO-US017391.
 XX PR 31-MAY-2000; 2000US-0208451P.
 PR 02-AUG-2000; 2000US-00631191.
 XX XX
 PA (GENV-) GENVEC INC.
 XX XX
 PI Wickham TJ, Kovesdi I, Roelvink PW, Einfield D, Brough DE;
 PI Lizonova A;
 XX XX
 DR WPI; 2002-147620/19.
 XX XX
 PT Adenoviral coat protein which permits production of adenoviral vectors
 PT that bind and infect host cells not naturally infected by adenovirus,
 comprises various non-native ligands.
 Claim 4; Page 40; 45pp; English.
 The invention relates to adenoviral coat proteins comprising various non-
 native ligands. The invention provides a method of controlled gene
 expression utilising selectively replication competence and also a method
 and a composition for targeting an adenoviral vector. A system
 comprising a cell having a non-native cell-surface receptor, and a virus
 having a non-native ligand which binds the non-native cell-surface
 receptor of the cell is useful for propagating a virus and also for
 assaying gene function. The system is also useful for isolating a nucleic
 acid encoding a product comprising a desired property. Further the system
 is useful for identifying functionally related coding sequences.
 CC Adenoviral vector comprising a non-native nucleic acid encoding a
 CC therapeutic agent such as anti-tumour agent, preferably tumour necrosis
 CC factor and a second non-native nucleic acid encoding an agent that
 CC facilitates imaging and a targeting agent is useful for treating an
 CC animal. The therapeutic agent can be used to treat cancer of the brain,
 CC lung, ovary, breast and prostate. The present sequence is human non-
 CC native ligand attached to an adenoviral vector
 XX SQ Sequence 5 AA;
 Query Match 100.0%; Score 35; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 DB |||||
 1 CRGDC 5
 RESULT 18
 ABUS9650
 ID ABUS9650 standard; peptide; 5 AA.
 XX AC ABUS9650;
 XX DT 22-APR-2003 (first entry)
 XX DE Fibronectin-binding integrin alpha5-beta1 targeting peptide #11.
 XX KW Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic;
 KW cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;
 KW fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
 KW tumour; cationic cancer-targeting peptide.
 XX OS Synthetic.
 XX PN US2002041898-A1.
 XX PD 11-APR-2002.
 XX PF 25-JUL-2001; 2001US-00912609.
 XX PR 05-JAN-2000; 2000US-00478124.
 PR 31-OCT-2000; 2000US-00703474.
 XX XX
 PA (UNGE/) UNGER E C.
 PA (MATS/) MATSUNAGA T O.
 PA (RAMA/) RAMASWAMI V.
 PA (ROMA/) ROMANOWSKI M J.
 XX XX
 PI Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;
 XX WPI; 2003-208921/20.
 XX XX
 PT Targeted delivery system comprising a bioactive agent homogeneously
 PT dispersed in a targeted matrix is especially useful in cancer therapy.
 XX PS Claim 42; Page 38; 46pp; English.
 XX XX

CC inexpensively synthesised

XX Sequence 5 AA;

Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5

Db 1 CRGDC 5

RESULT 14

ADE25491
 ID ADE25491 standard; peptide; 5 AA.

XX AC ADE25491;

XX DT 29-JAN-2004 (first entry)

XX DE Tc-99m labelled peptide #19.

XX KW Thrombus imaging agent; GPIIb/IIIa receptor; thrombus.

XX OS Synthetic.

XX XX US5888474-A.

XX PD 30-MAR-1999.

XX PF 07-JUN-1995; 95US-00478725.

XX PR 08-FEB-1991; 91US-00653012.

XX PR 27-NOV-1991; 91US-00807062.

XX PR 21-MAY-1992; 92US-00886752.

XX PR 22-JUN-1994; 94US-00264176.

XX PR 11-JUL-1994; 94US-00273274.

XX PR 07-JUN-1995; 95US-00480551.

XX PA (DIAT-) DIATIDE INC.

XX PI Dean RT, Lister-James J;

XX XX WPI; 1999-253220/21.

XX DR WPI; 1999-253220/21.

XX PT Reagent for preparing thrombus imaging agent.

XX PS Example 2; Col 12; 17pp; English.

XX CC The present invention relates to reagents (A) for preparing thrombus
 imaging agents comprising specific binding peptides (I) and a technetium-
 99m binding group (II) covalently attached to the specific binding
 peptide. (I) is a ligand for the GPIIb/IIIa receptor and can be a cyclic
 or linear peptide not containing the Arg-Gly-Asp (RGD) sequence. (I) are
 specific for thrombi, and are small and therefore are rapidly cleared
 from blood and background tissue. (A) are used to produce scintigraphic
 imaging agents for detection of thrombi in vivo. The present sequence is
 one such Tc-99m labelled peptide.

XX Sequence 5 AA;

Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5

Db 1 CRGDC 5

RESULT 15

AA54976

ID AA54976 standard; peptide; 5 AA.

XX AC AA54976;

XX DT 15-FEB-2000 (first entry)

XX DE Peptide ligand for fibrin polymerisation site.

XX KW Thrombus imaging; fibrin polymerisation site; technetium-99m; Tc-99m;
 GPIIb/IIIa receptor; cyclic peptide ligand.

XX OS Synthetic.

XX PN US5968476-A.

XX PD 19-OCT-1999.

XX PF 07-JUN-1995; 95US-00484773.

XX PR 21-MAY-1992; 92US-00886052.

XX PR 11-JUL-1994; 94US-00273274.

XX XX (DIAT-) DIATIDE INC.

XX PI Dean RT, Lister-James J;

XX XX WPI; 2000-021733/02.

XX PT A complex used for thrombus imaging comprises technetium-99m complexed
 with a peptide ligand for GPIIb/IIIa receptor.

XX PS Example 2; Col 13-14; 18pp; English.

XX CC This sequence represents a peptide ligand for the fibrin polymerisation
 site. The invention relates to a complex (A) for thrombus imaging
 comprises technetium-99m (Tc-99m) complexed with a reagent comprising a
 peptide (P) with 4 to 100 amino acids sequence and a Tc-99m binding
 moiety covalently bound to (P). (P) is selected from a linear peptide
 ligand for a GPIIb/IIIa receptor not comprising the amino acid sequence
 (arginine-glycine-aspartate); a peptide ligand for a polymerisation site
 of fibrin, and a cyclic peptide ligand for the GPIIb/IIIa receptor. The
 thrombus imaging reagents provided by the present invention can be used
 for visualising thrombi in a mammalian body when Tc-99m is labelled

XX Sequence 5 AA;

Query Match 100.0%; Score 35; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5

Db 1 CRGDC 5

RESULT 16

AA54976

ID AA54976 standard; peptide; 5 AA.

XX AC AA54976;

XX DT 10-OCT-2000 (first entry)

XX DE GPIIb/IIIa receptor ligand.

XX KW Thrombus; imaging; radioimaging; thrombosis; thromboembolism; embolism;
 diagnosis; technetium-99m; GPIIb/IIIa receptor ligand.

XX OS Synthetic.

XX PN US6083481-A.

XX XX 04-JUL-2000.

RESULT 9
 AAW03492
 ID AAW03492 standard; peptide; 5 AA.
 XX AC AAW03492;
 XX DT 25-MAR-2003 (revised)
 DT 24-OCT-1996 (first entry)
 XX DT
 XX DE Alpha(5)-Beta(1) integrin binding peptide 10.
 XX KW Synthetic; fibronectin; vitronectin; integrin; binding motif; adhesion;
 KW extracellular matrix protein; tumour metastasis.
 XX OS Synthetic.
 XX PN US5536814-A.
 XX PD 16-JUL-1996.
 XX PF 11-MAR-1994; 94US-00212186.
 XX PR 27-SEP-1993; 93US-00127422.
 XX PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX PI Koivunen E, Ruoslahti E;
 DR WPI; 1996-341556/34.
 XX Synthetic integrin-binding peptide(s) - useful for inhibiting tumour
 PT metastasis, etc.
 XX PS Disclosure; Col 2; 16pp; English.
 CC Peptides AAW03483-508 are examples of synthetic peptides generated to
 CC bind to the fibronectin/vitronectin-binding integrin alpha(5)beta(1).
 CC They are synthesised to contain the alpha(5)beta(1)-integrin peptide
 CC binding motifs: DGR, NGR or RGD. The peptides interfere with the binding
 CC of fibronectin and vitronectin to this integrin and thus may be used to
 CC block integrin-mediated cell adhesion to extracellular matrix proteins,
 CC esp. to inhibit tumour metastasis. (Updated on 25-MAR-2003 to correct PF
 CC field.)
 XX SQ Sequence 5 AA;
 Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 DB |||||
 1 CRGDC 5
 RESULT 10
 AAW48499
 ID AAW48499 standard; peptide; 5 AA.
 XX AC AAW48499;
 XX DT 18-AUG-1998 (first entry)
 XX DE Integrin receptor antagonist peptide 38.
 XX KW Integrin receptor antagonist; cell adhesion modulator; leukocyte;
 KW extracellular matrix; fibronectin; ARDS; thrombosis; inflammation.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Disulfide-bond 1..5
 RESULT 11
 AAW64952
 ID AAW64952 standard; peptide; 5 AA.
 XX AC AAW64952;
 XX DT 25-MAR-2003 (revised)
 DT 23-SEP-1998 (first entry)
 XX DE Targetting peptide #45 useful as component of thrombolytic agent.
 XX KW Thrombolytic agent; thrombolytic proteinase; blood clot; fibrin;
 KW thrombus; antithrombotic activity.
 XX OS Synthetic.
 XX PN WO9824917-A1.
 XX PD 11-JUN-1998.
 XX PF 02-DEC-1997; 97WO-US021918.
 XX PR 02-DEC-1996; 96US-00753781.
 XX

US5721210-A.
 24-FEB-1998.
 07-JUN-1995; 95US-00485019.
 09-JUL-1990; 90US-00550330.
 09-JUL-1991; 91WO-US004862.
 04-JUN-1993; 93US-00961889.
 (TANA) TANABE SEIYAKU CO.
 Cardarelli PM, Lobl TJ, Chiang S;
 WPI; 1998-168442/15.
 New cyclic peptide(s) and peptidomimetic compounds - are integrin
 receptor antagonists useful in modulating cell adhesion.
 Example 9; Col 42; 32pp; English.
 The present sequence represents a synthetic peptide which acts as an
 antagonist to integrin receptors. The invention provides various
 synthetic peptides which act as cell adhesion modulators because they
 mimic extra-cellular matrix ligands or other cell adhesion ligands that
 bind to receptors such as integrin receptors, including fibronectin,
 laminin, LFA-1, MAC-1, p150,95, vitronectin and gp1b/IIb receptors.
 Some of the peptides contain the amino acid sequence Arg-Gly-Asp (RGD).
 Others contain non-RGD sequences, for e.g RCD sequences, and reverse
 orientation forms of amino acid residues. The synthetic peptides are
 useful in modulating cell adhesion, including adhesion related to
 fibronectin, as well as leukocyte adhesion to endothelial cells. They are
 also claimed to be useful in the study, diagnosis, treatment or
 prevention of diseases which relate to cell adhesion, e.g. adult
 respiratory distress syndrome (ARDS), thrombosis and inflammatory
 conditions
 Sequence 5 AA;
 Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDC 5
 DB |||||
 1 CRGDC 5
 RESULT 11
 AAW64952
 ID AAW64952 standard; peptide; 5 AA.
 XX AC AAW64952;
 XX DT 25-MAR-2003 (revised)
 DT 23-SEP-1998 (first entry)
 XX DE Targetting peptide #45 useful as component of thrombolytic agent.
 XX KW Thrombolytic agent; thrombolytic proteinase; blood clot; fibrin;
 KW thrombus; antithrombotic activity.
 XX OS Synthetic.
 XX PN WO9824917-A1.
 XX PD 11-JUN-1998.
 XX PF 02-DEC-1997; 97WO-US021918.
 XX PR 02-DEC-1996; 96US-00753781.
 XX

XX WPI; 1992-313678/38.
 XX New synthetic peptide lipids or salts - useful as cell migration
 PT inhibitors, cell adhesion membranes and cell culture bodies.
 XX Disclosure; Page 3; 9pp; Japanese.
 XX The peptide sequence is an example of a highly generic sequence contg.
 CC the RGD motif. Compounds contg. these lipid peptides are useful as cell
 CC migration inhibitors in cell adhesion membranes or cell culture bodies.
 CC See also AAR29048-54
 XX Sequence 5 AA;
 SQ

Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CRGDC 5
 |||||
 1 CRGDC 5

QY 1 CRGDC 5
 DB 1 CRGDC 5

RESULT 8
 AAR79093
 ID AAR79093 standard; peptide; 5 AA.
 AC AAR79093;
 DT 24-JAN-1996 (first entry)
 XX Alpha5/betal integrin binding peptide #20.
 XX High affinity; integrin binding peptide; alphas/betal; alphav/betas;
 KW alphav/betas3; RGD; stable configuration; wound healing;
 KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;
 KW smooth muscle cell migration.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..5
 XX WO9514714-A1.
 PN 01-JUN-1995.
 PD 22-NOV-1994; 94WO-US013542.
 PF 24-NOV-1993; 93US-00159001.
 PR 04-AUG-1994; 94US-00286861.
 XX (LJOL-) LA JOLLA CANCER RES FOUND.
 PA Ruoslahti E, Koivunen E;
 PI WPI; 1995-206899/27.
 DR
 XX High affinity integrin binding peptides - can be used to attach cells to
 a substrate, inhibit the attachment of osteoclasts to bone, promote wound
 PT healing, inhibit angiogenesis, metastasis of tumours and migration of
 PT smooth muscle cells.
 XX Example 3; Page 25; 86pp; English.
 PS The sequences given in AAR76185-200 and AAR79073-94 are high affinity
 CC integrin binding peptides which bind to various integrins. Peptides which
 CC bind to alphas/betal integrins contain the motifs given in AAR76185-86
 CC and peptides which bind to alphav/betas and alphav/betas3 integrins
 CC contain the motif given in AAR76187. Alphav/betas integrins are also
 CC bound by RGD containing peptides. These peptides assume a
 CC conformationally stabilised configuration which is due to the formation
 CC of a disulphide bond, a peptide bond or a lactam bond. These peptides may
 CC be used for isolating the complementary integrin from a sample mixture by
 CC contacting them under ionic conditions to allow binding of the integrin
 CC to the peptide and then separating the integrin from the peptide. They
 CC can be used for attaching cells to a substrate, by binding them to the
 CC substrate with the cell. The peptides promote wound healing when applied
 CC locally and inhibit the attachment of osteoclasts to bone. They inhibit
 CC angiogenesis, metastasis of tumours and migration of smooth muscle cells
 XX Sequence 5 AA;
 -SQ

Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CRGDC 5
 |||||
 1 CRGDC 5

QY 1 CRGDC 5
 DB 1 CRGDC 5

RESULT 7
 AAR69325
 ID AAR69325 standard; peptide; 5 AA.
 AC AAR69325;
 DT 25-MAR-2003 (revised)
 DT 25-JUN-1995 (first entry)
 XX Gp IIB/IIIA receptor ligand used in scintigraphic imaging of thrombi.
 DE Scintigraphy; thrombus; thrombi; imaging; specific binding;
 KW technetium-99m; radiolabelled; Gp IIB/IIIA receptor ligand.
 XX Synthetic.
 OS
 XX WO9323085-A1.
 PN 25-NOV-1993.
 PD 21-MAY-1993; 93WO-US004794.
 PF 21-MAY-1992; 92US-00886752.
 PR (DIAT-) DIATECH INC.
 PA Dean RT, Lister-James J;
 PI WPI; 1993-386229/48.
 DR Reagent for scintigraphic imaging of thrombi with 99m technetium -
 PT comprises synthetic peptide which binds to thrombus covalently coupled to
 PT metal binding gp., rapidly cleared from blood and tissue.
 XX Claim 41; Page 46; 61pp; English.
 PS The invention relates to reagents for scintigraphic imaging of a thrombus
 CC in-vivo, comprising (A) a specific binding compound capable of binding to
 CC at least one component of a thrombus, covalently linked to (B) a
 CC technetium-99m-binding moiety. Specific peptides constituting the
 CC reagents are claimed as new. The present peptide is one such peptide.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 5 AA;
 SQ

Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CRGDC 5
 |||||
 1 CRGDC 5

QY 1 CRGDC 5
 DB 1 CRGDC 5

XX 10-APR-1991 (first entry)
XX Fibrinogen receptor antagonising peptide (VI).
XX Fibrinogen receptor antagonist; platelet aggregation; thrombosis;
XX myocardial infarction.
XX Synthetic.
XX Key Location/Qualifiers
FH Disulfide-bond 1:..5
FT Modified-site 1:..1
FT /label= homoCys
XX
XX PN EP410537-A.
XX PD 30-JAN-1991.
XX 23-JUL-1990; 90EP-00202015.
XX 28-JUL-1989; 89US-00386534.
XX (MERI) MERCK & CO INC.
XX Nutt RF, Brady SF, Veber DF;
XX WPI; 1991-030928/05.
XX New fibrinogen receptor antagonising peptide cpds. - used to inhibit
PT blood platelet aggregation during surgery on peripheral arteries and in
PT cardiovascular surgery.
XX
XX Claim 7; Page 10; 10pp; English.
XX To residue homoCys1 is attached Acetyl and to residue Cys5 is attached
CC NH2. The peptide is prepd. using standard methods of solid phase
CC synthesis and is one of 17 pref. examples of a highly generic formula.
CC The peptide is used to inhibit fibrinogen-induced platelet aggregation
CC and is partic. useful because it does not significantly deplete the
CC platelet count. It has a relatively short duration of activity and is
CC thus useful where prevention of platelet aggregation over a short period
CC of time is desirable, e.g. in surgery of peripheral arteries and
CC cardiovascular surgery. It is also useful in prevention of platelet
CC thrombosis, thromboembolism and reocclusion either during and after
CC thrombolytic therapy, or after angioplasty of coronary and other arteries
CC and after coronary artery by-pass procedures, or to prevent myocardial
CC infarction. It may be combined with thrombolytic agents, e.g. plasminogen
CC activators or streptokinase, or anticoagulants. See also AAR10413-18 and
CC EP-410537, EP-410539, EP-410540, EP-410541, and EP-410767
XX
XX Sequence 5 AA;
Query Match 100.0%; Score 35; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDC 5
DB 1 CRGDC 5
RESULT 5
AAR27031
ID AAR27031 standard; peptide; 5 AA.
XX
XX AAR27031;
XX
XX 20-MAY-1998 (first entry)
XX Peptide lipid contg. RGD.
XX Synthetic; cell migration; inhibitor; cell adhesion membrane;

KW cell culture body.
XX Synthetic.
XX Key Location/Qualifiers
FH modified_site 1
FT /note= "acylated"
FT modified_site 5
FT /note= "alkylated"
XX
XX JP04221395-A.
XX 11-AUG-1992.
XX 29-NOV-1990; 90JP-00333336.
XX 26-OCT-1990; 90JP-00289494.
XX (FUJF) FUJI PHOTO FILM CO LTD.
XX WPI; 1992-313679/38.
XX New synthetic peptide lipid(s) and salts - useful as cell migration
PT inhibitors, cell adhesion membranes or cell culture bodies.
XX Disclosure; Page 3; 9pp; Japanese.
XX The peptide sequence is an example of a highly generic sequence contg.
CC the RGD motif. Compounds contg. these lipid peptides are useful as cell
CC migration inhibitors in cell adhesion membranes or cell culture bodies.
CC See also AAR27027-33
XX
XX Sequence 5 AA;
Query Match 100.0%; Score 35; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDC 5
DB 1 CRGDC 5
RESULT 6
AAR29052
ID AAR29052 standard; peptide; 5 AA.
XX
XX AAR29052;
XX 20-MAY-1998 (first entry)
XX Peptide lipid contg. RGD.
XX Synthetic; cell migration; inhibitor; cell adhesion membrane;
XX cell culture body.
XX Synthetic.
XX Key Location/Qualifiers
FH modified_site 1
FT /note= "acylated"
FT modified_site 5
FT /note= "alkylated"
XX
XX JP04221394-A.
XX 11-AUG-1992.
XX 29-NOV-1990; 90JP-00333335.
XX 26-OCT-1990; 90JP-00289493.
XX (FUJF) FUJI PHOTO FILM CO LTD.
XX

Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 DB 1 CRGDC 5

RESULT 2
 AAR10415
 ID AAR10415 standard; protein; 5 AA.

AC AAR10415;
 DT 10-APR-1991 (first entry)
 DE Fibrinogen receptor antagonising peptide (III).
 KW Fibrinogen receptor antagonist; platelet aggregation; thrombosis;
 KW myocardial infarction.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Disulfide-bond 1..5
 FT Modified-site 1..1
 FT /label= N-MethylCys

PN EP410537-A.
 XX 30-JAN-1991.

PF 23-JUL-1990; 90EP-00202015.
 PR 28-JUL-1989; 89US-00386534.
 XX (MERI) MERCK & CO INC.

PI Nutt RF, Brady SF, Veber DF;
 WPI; 1991-030928/05.

XX New fibrinogen receptor antagonising peptide cpds. - used to inhibit
 PT blood platelet aggregation during surgery on peripheral arteries and in
 PT cardiovascular surgery.

PS Claim 5; Page 10; 10pp; English.

XX To residue N-MethylCys1 is attached Acetyl and to residue Cys5 is
 CC attached OH. The peptide is prepd. using standard methods of solid phase
 CC synthesis and is one of 17 pref. examples of a highly generic formula.
 CC The peptide is used to inhibit fibrinogen-induced platelet aggregation
 CC and is partic. useful because it does not significantly deplete the
 CC platelet count. It has a relatively short duration of activity and is
 CC thus useful where prevention of platelet aggregation over a short period
 CC of time is desirable, e.g. in surgery of peripheral arteries and
 CC cardiovascular surgery. It is also useful in prevention of platelet
 CC thrombosis, thromboembolism and reocclusion either during and after
 CC thrombolytic therapy, or after angioplasty of coronary and other arteries
 CC and after coronary artery by-pass procedures, or to prevent myocardial
 CC infarction. It may be combined with thrombolytic agents, e.g. plasminogen
 CC activators or streptokinase, or anticoagulants. See also AAR10413-18 and
 CC EP-410537, EP-410539, EP-410540, EP-410541, and EP-410767

XX Sequence 5 AA;

Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 DB 1 CRGDC 5

Db 1 CRGDC 5

RESULT 3

ID AAR10414 standard; protein; 5 AA.

AC AAR10414;

DT 10-APR-1991 (first entry)

DE Fibrinogen receptor antagonising peptide (II).

KW Fibrinogen receptor antagonist; platelet aggregation; thrombosis;
 KW myocardial infarction.

OS Synthetic.

FT Key Location/Qualifiers
 FT Disulfide-bond 1..5

PN EP410537-A.

PD 30-JAN-1991.

PF 23-JUL-1990; 90EP-00202015.

PR 28-JUL-1989; 89US-00386534.

XX (MERI) MERCK & CO INC.

PI Nutt RF, Brady SF, Veber DF;

WPI; 1991-030928/05.

PT New fibrinogen receptor antagonising peptide cpds. - used to inhibit
 PT blood platelet aggregation during surgery on peripheral arteries and in
 PT cardiovascular surgery.

PS Claim 4; Page 10; 10pp; English.

XX To residue Cys5 is attached OH. The peptide is prepd. using standard
 CC methods of solid phase synthesis and is one of 17 pref. examples of a
 CC highly generic formula. The peptide is used to inhibit fibrinogen-induced
 CC platelet aggregation and is partic. useful because it does not
 CC significantly deplete the platelet count. It has a relatively short
 CC duration of activity and is thus useful where prevention of platelet
 CC aggregation over a short period of time is desirable, e.g. in surgery of
 CC peripheral arteries and cardiovascular surgery. It is also useful in
 CC prevention of platelet thrombosis, thromboembolism and reocclusion either
 CC during and after thrombolytic therapy, or after angioplasty of coronary
 CC and other arteries and after coronary artery by-pass procedures, or to
 CC prevent myocardial infarction. It may be combined with thrombolytic
 CC agents, e.g. plasminogen activators or streptokinase, or anticoagulants.
 CC See also AAR10413-18 and EP-410537, EP-410539, EP-410540, EP-410541, and
 CC EP-410767

XX Sequence 5 AA;

Query Match 100.0%; Score 35; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
 DB 1 CRGDC 5

RESULT 4

ID AAR10418 standard; protein; 5 AA.

AC AAR10418;

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OM protein - protein search, using sw model

Run on: September 22, 2004, 07:48:21 / Search time 121 Seconds
(without alignments)
11.676 Million cell updates/sec

Title: US-09-912-609-9
Perfect score: 35
Sequence: 1 CRGDC 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 34717

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A-Geneseq_29Jan04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	5	2 AAR1587	Aar1587 Fibrinoge
2	35	100.0	5	2 AAR10415	Aar10415 Fibrinoge
3	35	100.0	5	2 AAR10414	Aar10414 Fibrinoge
4	35	100.0	5	2 AAR10418	Aar10418 Fibrinoge
5	35	100.0	5	2 AAR27031	Aar27031 Peptide 1
6	35	100.0	5	2 AAR29052	Aar29052 Peptide 1
7	35	100.0	5	2 AAR69325	Aar69325 Gp IIB/II
8	35	100.0	5	2 AAR79093	Aar79093 Alpha5/be
9	35	100.0	5	2 AA003492	AA003492 Alpha(5)-
10	35	100.0	5	2 AA048499	AA048499 Integrin
11	35	100.0	5	2 AA064952	AA064952 Targettin
12	35	100.0	5	2 AA050594	AA050594 GPIIb/III
13	35	100.0	5	2 AA021570	AA021570 Integrin-
14	35	100.0	5	2 ADE25491	Ade25491 TC-99m la
15	35	100.0	5	3 AAY54976	Aay54976 Peptide 1
16	35	100.0	5	3 AAY95465	Aay95465 GPIIb/III
17	35	100.0	5	5 AAE17982	Aae17982 Human lig
18	35	100.0	5	6 ABUS9650	Abu9650 Fibrinoc
19	32	91.4	5	2 AAY16025	Aay16025 Snake ven
20	30	85.7	5	3 AAO22876	Aao22876 Angiogeni
21	30	85.7	5	4 AAB97087	Aab97087 Integrin-
22	30	85.7	5	5 ABP54052	Abp54052 Alpha-v-b
23	30	85.7	5	5 ABG70730	Abg70730 avB5 bind
24	30	85.7	5	5 AAU79139	Aau79139 Synthetic
25	30	85.7	5	5 AAG78428	Aag78428 Cyclic pe

26	30	85.7	5	6 ABG73025	Abg73025 Integrin
27	30	85.7	5	6 ABP60344	Abp60344 Tumour va
28	28	80.0	5	2 AAR31385	Aar31385 Cyclic pl
29	28	80.0	5	2 AAR31389	Aar31389 Cyclic pl
30	28	80.0	5	2 AAR31384	Aar31384 Cyclic pl
31	28	80.0	5	2 AAR31395	Aar31395 Cyclic pl
32	28	80.0	5	2 AAR31400	Aar31400 Cyclic pl
33	28	80.0	5	2 AAR31404	Aar31404 Cyclic pl
34	28	80.0	5	2 AAR31394	Aar31394 Cyclic pl
35	28	80.0	5	2 AAR31393	Aar31393 Cyclic pl
36	26	74.3	4	2 AAR11744	Aar11744 Cyclic pl
37	26	74.3	4	2 AAR11745	Aar11745 Cyclic pl
38	26	74.3	4	2 AAR24214	Aar24214 Fragment
39	26	74.3	4	2 AAR69324	Aar69324 Gp IIB/II
40	26	74.3	4	2 AAW25175	Aaw25175 RGD-pepti
41	26	74.3	4	2 AAW64951	Aaw64951 Targettin
42	26	74.3	4	3 AAY52481	Aay52481 Fibrinect
43	26	74.3	4	3 AAY80468	Aay80468 Cell adhe
44	26	74.3	4	3 AAY95464	Aay95464 GPIIb/III
45	26	74.3	4	4 AAB91949	Aab91949 Fibrinect

ALIGNMENTS

RESULT 1
AAR1587
ID AAR1587 standard; protein; 5 AA.
XX AC AAR1587;
XX 12-JUN-1991 (first entry)
XX DE Fibrinogen receptor antagonist #4.
XX KW fibrinogen receptor antagonist; thrombosis; fibrinogen;
XX KW IIB/IIIA receptor.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Disulfide-bond 1..5
FT Modified-site 2
FT /label= Arg(phenyl)
XX EP422938-A.
XX 17-APR-1991.
XX 11-OCT-1990; 90BP-00311151.
XX 13-OCT-1989; 89US-00421224.
XX (MERI) MERCK & CO INC.
XX Nutt RF, Brady ST, Veber KF, Duggan MF;
XX WPI; 1991-111423/16.
XX Polypeptide fibrinogen receptor antagonists - used to prevent thrombosis,
XX e.g. during cardiovascular surgery.
XX Disclosure; Page 7; 16pp; English.
XX Cys at position 1 carries an acetyl group. The peptide inhibits binding
XX of fibrinogen to the platelet membrane glycoprotein complex IIB/IIIA
XX receptor. It may be used to prevent post-operative thrombosis,
XX thromboembolism and reocclusion, platelet adhesion in extracorporeal
XX blood circulation systems and to prevent myocardial infarction. See also
XX AAR11584-6 and AAR11588-R11594
XX Sequence 5 AA;
SQ

OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RC SEQUENCE, AND SYNTHESIS.
 RP TISSUE=Brain;
 RX PubMed=613771;
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by
 antibodies to FMRamide.";
 RL Nature 305:328-330(1983).
 CC - FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC - SIMILARITY: BELONGS TO THE FARP (PMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW GO:0007218; P:neuropeptide signaling pathway; TAS.
 DR Neuropeptide; Amidation.
 FT MOD RES 5
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;
 AMIDATION.
 Query Match 14.3%; Score 5; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. NO. 1e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 R 2
 DB 4 R 4
 RESULT 4
 P83568 PRELIMINARY; PRT; 4 AA.
 AC P83568;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Pheromone peptide ILME.
 OS Sepia officinalis (Common cuttlefish).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
 OX NCBI_TaxID=6610;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
 RP SPECTROMETRY.
 RC TISSUE=Egg;
 RX PubMed=10944467;
 RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
 RT "ILME: a waterborne pheromonal peptide released by the eggs of Sepia
 officinalis.";
 RL Biochem. Biophys. Res. Commun. 275:217-222(2000).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Egg;
 RX PubMed=12207899;
 RA Zatylny C., Marvin L., Gagnon J., Henry J.;
 RT "Fertilization in Sepia officinalis: the first mollusk sperm-
 attracting peptide.";
 RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
 CC - FUNCTION: HAS MYOTROPIC ACTIVITY TARGETING THE GENITAL TRACT.
 CC - SUBCELLULAR LOCATION: SECRETED.
 CC - TISSUE SPECIFICITY: FOLLICLE, FULLY GROWN OOCYTE AND EGG(EC2).
 CC - MASS SPECTROMETRY: MW=505.4; METHOD=WALDI.
 DR GO:0005186; F:pheromone activity; IEA.
 KW Pheromone.
 SQ SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;
 Query Match 5.7%; Score 2; DB 5; Length 4;
 Best Local Similarity 0.0%; Pred. NO. 1e+06;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 D 4
 DB 4 E 4

RESULT 5
 Q08433 PRELIMINARY; PRT; 4 AA.
 AC Q08433;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Bilirubin UDP-glucuronosyltransferase (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Gunn;
 RX MEDLINE=91282758; PubMed=1840486;
 RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
 RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
 hyperbilirubinemic Gunn rat.";
 RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
 DR EMBL; S38636; AAB19259.1; -.
 DR GO:0016740; F:transferase activity; IEA.
 KW Transferase.
 FT NON_TER 1
 SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;
 Query Match 5.7%; Score 2; DB 11; Length 4;
 Best Local Similarity 0.0%; Pred. NO. 1e+06;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 R 2
 DB 4 K 4
 RESULT 6
 Q99007 PRELIMINARY; PRT; 5 AA.
 AC Q99007;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Alpha amylase (Fragment).
 GN AMY1 GENS.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91329704; PubMed=1831055;
 RA Jacobsen J.V., Close T.J.;
 RT "Control of transient expression of chimaeric genes by gibberellic
 acid and abscisic acid in protoplasts prepared from mature barley
 aleurone layers.";
 RL Plant Mol. Biol. 16:713-721(1991).
 DR EMBL; X54643; CAA38455.1; -.
 FT NON_TER 5
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;
 Query Match 5.7%; Score 2; DB 10; Length 5;
 Best Local Similarity 0.0%; Pred. NO. 1e+06;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 R 2
 DB 4 K 4

Search completed: September 22, 2004, 07:10:44
 Job time : 112 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2004, 07:02:58 ; Search time 111 seconds
(without alignments)
14.213 Million cell updates/sec

Title: US-09-912-609-9
Perfect score: 35
Sequence: 1 CRGDC 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organalle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	6	17.1	2	5 P83570	P83570 sepioid offic
2	6	17.1	5	2 P83073	P83073 bacillus ce
3	5	14.3	5	13 P83308	P83308 gallus gall
4	2	5.7	4	5 P83568	P83568 sepioid offic
5	2	5.7	4	11 Q08433	Q08433 rattus sp.
6	2	5.7	5	10 Q99007	Q99007 hordeum vul

ALIGNMENTS

RESULT 1
P83570
ID P83570 PRELIMINARY; PRT; 2 AA.
AC P83570;
DT 01-JUN-2003 (TRENBLrel. 24, Created)

DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Neuropeptide GWA.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RX TISSUE=Optic lobe;
RA Henry J., Favrel P., Boucaud-Camou E.;
RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related
RT peptide inhibiting the motility of the mature oviduct in the
RT cuttlefish, Sepia officinalis.";
RL Peptides 18:1469-1474(1997).
CC -!- FUNCTION: REGULATORY NEUROPEPTIDE WITH MYOTROPIC ACTIVITY
CC TARGETING THE DISTAL OVIDUCT. INHIBITS THE MOTILITY OF THE OVIDUCT
CC BY DECREASING TONUS, FREQUENCY AND AMPLITUDE OF CONTRACTIONS.
CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI.
DR GO: GO:0007218; P:neuropeptide signaling pathway; IEA.
KW Neuropeptide; Amidation.
FT MOD RES 2 2
SQ SEQUENCE 2 AA; 261 MW; 7378100000000000000 CRC64;

Query Match 17.1%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3
Db 1 G 1

RESULT 2

P83073
ID P83073 PRELIMINARY; PRT; 5 AA.
AC P83073;
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE 88 kDa protein (fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE
RA STRAIN=NCIMB 11796;
RA Browne N., Dowds B.C.A.;
RL Submitted (JUL-2001) to Swiss-Prot.
FT NON TER 5 5
SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 17.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 D 4
Db 3 D 3

RESULT 3

P83308
ID P83308 PRELIMINARY; PRT; 5 AA.
AC P83308;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE FMRFamide-like neuropeptide (LFLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M21922; -; NOT_ANNOTATED_CDS.
CC DR PIR; I40697; I40697.
CC DR InterPro; IP0005814; AminoTrans 3.
CC DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
CC KW Biotin biosynthesis; Transferase; Aminotransferase;
CC FT Pyridoxal phosphate.
CC FT NON TER 5
CC SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 17.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 D 4
Db 4 D 4

RESULT 13
PAP2_PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moses sole).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
CC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
CC Soleiidae; Soleidae; Pardachirus.
CC NCBI_TaxID=31087;
CC [1]
CC RP SEQUENCE.
CC RC TISSUE=Skin secretion;
CC RX MEDLINE=87057369; PubMed=3782138;
CC RA Lazarovici P., Primor N., Loew L.M.;
CC "Purification and pore-forming activity of two hydrophobic
CC RT polypeptides from the secretion of the Red sea moses sole (Pardachirus
CC RT marmoratus).";
CC RL J. Biol. Chem. 251:16704-16713(1986).
CC CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pardaxin family.
CC Toxin.
CC KW NON TER 5
CC FT NON TER 5
CC SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 17.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3
Db 1 G 1

RESULT 14
RE11_LITRU STANDARD; PRT; 5 AA.
AC P82070;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rubellidin 1.1.
OS Litoria rubella (Desert tree frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;

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CC Pelodyadinae; Litoria.
CC OX NCBI_TaxID=104895;
CC [1]
CC RP SEQUENCE, AND MASS SPECTROMETRY.
CC RC TISSUE=Skin secretion;
CC RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
CC Tyler M.J., Wallace J.C.;
CC RT "The structure of new peptides from the Australian red tree frog
CC RT 'Litoria rubella'. The skin peptide profile as a probe for the study
CC RT of evolutionary trends of amphibians.";
CC RL Aust. J. Chem. 49:955-963(1996).
CC CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC CC -!- MASS SPECTROMETRY: MW=598; METHOD=FAE.
CC KW Amphibian defense peptide.
CC SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 17.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 D 4
Db 2 D 2

RESULT 15
RE32_LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
CC Pelodyadinae; Litoria.
CC OX NCBI_TaxID=104895;
CC [1]
CC RP SEQUENCE.
CC RC TISSUE=Skin secretion;
CC RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
CC RT "Peptides from the skin glands of the Australian buzzing tree frog
CC RT Litoria electrica. Comparison with the skin peptides from Litoria
CC RT rubella.";
CC RL Aust. J. Chem. 52:639-645(1999).
CC CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC KW Amphibian defense peptide.
CC SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 17.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3
Db 2 G 2

Search completed: September 22, 2004, 07:08:47
Job time : 23 secs

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DE Eosinophilotactic peptides.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE=76078412; PubMed=1060093;
RX MEDLINE=76078412; PubMed=1060093;
RA Goetzl E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilotactic tetrapeptides of
RT human lung tissue: identification as eosinophil chemotactic factor of
RT anaphylaxis."
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -!- MISCELLANEOUS: These peptides are released from mast cells in lung
CC (and other tissues) during hypersensitivity reactions
CC (anaphylaxis). Their activities, preferentially affecting
CC eosinophils, include chemotaxis, chemotactic deactivation, release
CC of enzymes, and stimulation of the hexose monophosphate shunt.
DR GO:0006935; P:chemotaxis; IDA.
DR GO:0006955; P:immune response; IDA.
FT VARIANT 1 V -> A (IN OTHER PEPTIDE).
FT /FTID=VAR 005201.
SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match 17.1%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 G 3
DB 2 G 2

RESULT 10
OCP3 OCTMI STANDARD; PRT; 4 AA.
AC P58649.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Octopus minor (Octopus)
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor."
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-4 is a 1000 time less
CC active than Ocp-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=WALDI.
KW Hormone; D-amino acid.
FT MOD_RES 2 D-SERINE (IN OCP-4).
FT SEQUENCE 4 AA; 463 MW; 6AB365B910000000 CRC64;

Query Match 17.1%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 G 3
DB 1 G 1

RESULT 11

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ALL14 CARMA STANDARD; PRT; 5 AA.
ID AL14 CARMA
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinostatin 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]_TaxID=6759;
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 5 AMIDATION (POTENTIAL).
FT SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 17.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 G 3
DB 4 G 4

RESULT 12
BIOA CITFR STANDARD; PRT; 5 AA.
ID BIOA CITFR
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxonanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
GN BIOA.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;
RA Shian D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons."
RL Gene 67:203-211(1988).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxonanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC diaminonanoate.
CC -!- COFACTOR: Pyridoxal phosphate.
CC -!- PATHWAY: Biotin biosynthesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC aminotransferases.
CC -----
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CC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91072226; PubMed=2254256;
 RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
 RT "A new *Vibrio fischeri* lux gene precedes a bidirectional termination
 site for the lux operon.";
 RL J. Bacteriol. 172:6797-6802(1990).
 CC -!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
 CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
 CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
 CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
 CC -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
 CC an acyl-protein thioester.
 CC -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
 CC -----
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 CC -----
 DR EMBL; M62812; -; NOT ANNOTATED_CDS.
 KW Luminescence; Ligase.
 FT NON TER 1
 SQ SEQUENCE 3 AA; 374 MW; 6AA330303000000000 CRC64;
 Query Match 17.1%; Score 6; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 D 4
 Db 3 D 3
 RESULT 7
 ACH1 ACHFU
 ID ACH1 ACHFU STANDARD; PRT; 4 AA.
 AC P35904;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Achatin-I
 OS Achatina fulica (Giant African snail).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 CC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 RC STRAIN=Perussac; TISSUE=Ganglion;
 RX MEDLINE=89273551; PubMed=2597281;
 RA Kanatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 RT fulica Ferussac containing a D-amino acid residue.";
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=Perussac; TISSUE=Heart atrium;
 RX MEDLINE=91264856; PubMed=1675568;
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
 RT "Purification of achatin-I from the atria of the African giant snail,
 RT Achatina fulica, and its possible function.";
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=93014529; PubMed=1399265;

RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
 RA Iwashita T., Nomoto K.;
 RT "Crystal structure and molecular conformation of achatin-I
 RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
 RT D-amino acid residue.";
 RL Int. J. Pept. Protein Res. 39:258-264(1992).
 CC -!- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency
 CC and produces a spike broadening of the identified heart excitatory
 CC neuron (PON); also enhances the amplitude and frequency of the
 CC heart beat. Has also an effect on several other muscles.
 DR PIR; A32480; A32480.
 KW Hormone; D-amino acid.
 FT MOD RES 2
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;
 Query Match 17.1%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 G 3
 Db 1 G 1
 RESULT 8
 DCML PSECH
 ID DCML PSECH STANDARD; PRT; 4 AA.
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit L) (CO-DH L) (Fragment).
 GN CUTL.
 OS Pseudomonas carboxydohydrogena.
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Bradyrhizobiaceae.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydohydrogenic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -!- COFACTOR: Molybdenum (molybdopterin).
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR; P0140; P0140.
 KW Oxidoreductase; Molybdenum.
 FT NON TER 4
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F0F0000000 CRC64;
 Query Match 17.1%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 G 3
 Db 2 G 2
 RESULT 9
 EOSI HUMAN
 ID EOSI HUMAN STANDARD; PRT; 4 AA.
 AC P02731;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)


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Query Match      34.3%; Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GD 4
DB      3 GD 4

RESULT 3
TRM3 ECOLI
ID TRM3 ECOLI STANDARD; PRT; 5 AA.
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tram protein (Fragment).
GN TRAM.
OS Escherichia coli.
OG Plasmid IncFII R100.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88227859; PubMed=2836369;
RA Inamoto S., Yoshioka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the traJ
RT and traY genes of plasmid R100.";
RL J. Bacteriol. 170:2749-2757(1988).
CC -!- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the tra family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; M20941; -; NOT ANNOTATED_CDS.
DR PIR; A32014; A32014.
DR Conjugation; Plasmid; DNA-binding.
FT NON_TER 1
SQ SEQUENCE 5 AA; 634 MW; 6B1B1AA43500000 CRC64;

Query Match      22.9%; Score 8; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 RGD 4
DB      1 RND 3

RESULT 4
TPIS CANFA
ID TPIS CANFA STANDARD; PRT; 5 AA.
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
GN TPIS.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.

TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
CC phosphate.
CC -!- PATHWAY: Plays an important role in several metabolic pathways.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the triosephosphate isomerase family.
DR HSC-2DPAGE; P54714; DOG.
DR InterPro; IPR000852; Triophos_ismrse.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 1
FT NON_TER 5
SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match      20.0%; Score 7; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 GD 4
DB      3 GN 4

RESULT 5
GRWM HUMAN
ID GRWM HUMAN STANDARD; PRT; 3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experientia 33:324-325(1977).
CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate
CC growth of some cell types and to inhibit other types in vitro.
DR GO; GO:0001558; P:regulation of cell growth; NAS.
SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match      17.1%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 G 3
DB      1 G 1

RESULT 6
LUXE VIBFI
ID LUXE VIBFI STANDARD; PRT; 3 AA.
AC P24372;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE protein synthetase) (Fragment).
GN LUXE.
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

```

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OM protein - protein search, using sw model

Run on: September 22, 2004, 07:02:23 ; Search time 22 Seconds
(without alignments)
11.834 Million cell updates/sec

Title: US-09-912-609-9
Perfect score: 35
Sequence: 1 CRGDC 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	12	34.3	4	1	OCPL OCTMI	P58648 octopus min
2	12	34.3	5	1	UXA4 CHLTR	P38005 chlamydia t
3	8	22.9	5	1	TRN3 SCOLI	P13973 escherichia
4	7	20.0	5	1	TPIS CANFA	P54714 canis famil
5	6	17.1	3	1	GRWM HUMAN	P01157 homo sapien
6	6	17.1	3	1	LUXE VIBFI	P24272 vibrio fisci
7	6	17.1	4	1	ACH1 ACHFU	P35904 achatina fu
8	6	17.1	4	1	DCML PSECH	P19916 pseudomonas
9	6	17.1	4	1	ECST HUMAN	P02731 homo sapien
10	6	17.1	4	1	OCPL OCTMI	P58649 octopus min
11	6	17.1	5	1	AL14 CARMA	P81817 carcinus ma
12	6	17.1	5	1	BIOA CITPR	P13071 citrobacter
13	6	17.1	5	1	PAP2 PARMA	P81864 pardachirus
14	6	17.1	5	1	RE11 LITRU	P82070 litoria rub
15	6	17.1	5	1	RE32 LITRU	P82073 litoria rub
16	6	17.1	5	1	UF01 MOUSE	P38639 mus musculu
17	5	14.3	4	1	FAR3 HIRME	P42563 hirudo medi
18	5	14.3	4	1	FAR3 HIRME	P42563 hirudo medi
19	5	14.3	4	1	FLRF HIRME	P42561 hirudo medi
20	5	14.3	4	1	FLRN ANTEL	P58707 anthopleura
21	5	14.3	4	1	FNRF MACNI	P01162 macrocallis
22	5	14.3	4	1	FYRI ANTEL	P58706 anthopleura
23	5	14.3	4	1	TUFT HUMAN	P01858 homo sapien
24	5	14.3	5	1	FARP ARTRR	P41853 artiposthi
25	5	14.3	5	1	PRCT PERAM	P01373 triplaneta
26	2	5.7	4	1	DCMS PSECH	P19918 pseudomonas
27	2	5.7	4	1	FKFA ANTEL	P58705 anthopleura
28	2	5.7	5	1	BP77 BOTIN	P30425 bothrops in
29	2	5.7	5	1	RE21 LITRU	P82071 litoria rub
30	2	5.7	5	1	RE31 LITRU	P82072 litoria rub
31	2	5.7	5	1	UC22 MAIZE	P80628 zea mays (m
32	1	2.9	3	1	THYL PIG	P01151 sus scrofa
33	1	2.9	5	1	PSK DAUCA	P58261 daucus caro

34 0 0.0 4 1 RM01 YEAST P36515 saccharomyc
35 0 0.0 5 1 BIOB CITPR P2997 citrobacter
36 0 0.0 5 1 E103 LITRU P82099 litoria rub
37 0 0.0 5 1 E104 LITRU P82100 litoria rub
38 0 0.0 5 1 SUGA_ACHDO P19991 acheta dome

ALIGNMENTS

RESULT 1
OCPL OCTMI
ID OCPL OCTMI STANDARD; PRT; 4 AA.
AC P58648;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cardioactive peptides Ocp-1/Ocp-2.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-2 is a 1000 time less
CC active than Ocp-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PFM: Ocp-2 has L-Phe instead of D-Phe.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW Hormone; D-amino acid.
FT MOD RES 2 2 D-PHENYLALANINE (IN OCP-1).
SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;

Query Match 34.3%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 GD 4
Db 3 GD 4

RESULT 2
UXA4 CHLTR
ID UXA4 CHLTR STANDARD; PRT; 5 AA.
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/Bu;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christianten G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.;
RA Submitted (SEP-1994) to Swiss-Prot.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.5, ITS MW IS: 28 kDa.
DR Siena-2DPAGE; P38005; -
FT NON TER 5 5
SQ SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;

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OM protein - protein search, using sw model

Run on: September 22, 2004, 07:04:09 ; Search time 38 Seconds
(without alignments)
12.657 Million cell updates/sec

Title: US-09-912-609-9

Perfect score: 35

Sequence: 1 CRGDC 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	48.6	5	2 B45525	actin I - malaria
2	14	40.0	4	2 S43959	Ig mu chain V regi
3	14	40.0	5	2 F22565	R-phycoerythrin ga
4	12	34.3	4	2 PT0711	T-cell receptor be
5	12	34.3	5	2 PQ0689	photosystem I 10.4
6	12	34.3	5	2 PT0513	T-cell receptor be
7	12	34.3	5	2 PT0538	T-cell receptor be
8	12	34.3	5	2 PT0703	T-cell receptor be
9	12	34.3	5	2 PT0690	T-cell receptor be
10	12	34.3	5	2 PT0573	T-cell receptor be
11	12	34.3	5	2 PT0679	T-cell receptor be
12	11	31.4	4	2 S47552	ubiquitin - rat
13	11	31.4	4	2 S52238	pallidipin - assas
14	11	31.4	5	2 A33882	cadmium-binding pe
15	11	31.4	5	2 PT0525	T-cell receptor be
16	11	31.4	5	2 PT0608	T-cell receptor be
17	11	31.4	5	2 PT0695	T-cell receptor be
18	11	31.4	5	2 PT0700	T-cell receptor be
19	9	25.7	3	3 A22565	R-phycoerythrin al
20	9	25.7	4	2 IS1049	metallothionein-A
21	9	25.7	5	2 B22565	R-phycoerythrin al
22	9	25.7	5	2 S5726	hemoglobin, extrac
23	8	22.9	4	2 D41654	hypothetical prote
24	8	22.9	4	2 PT0677	T-cell receptor be
25	8	22.9	5	2 A32014	tram protein - Esc
26	8	22.9	5	2 PT0540	T-cell receptor be
27	7	20.0	3	3 A23751	spinal cord peptid
28	7	20.0	4	1 EXAAA	antho-RFamide neur
29	7	20.0	4	2 A25844	antho-RF amide neu

30	7	20.0	4	2 S09478	globulin IV alpha
31	6	17.1	3	3 GKHU	growth-modulating
32	6	17.1	3	3 A60898	bursin - chicken
33	6	17.1	3	3 B23751	spinal cord peptid
34	6	17.1	3	3 PT0636	T-cell receptor be
35	6	17.1	3	3 PT0571	T-cell receptor be
36	6	17.1	4	2 A32039	tyrosine-melanocyt
37	6	17.1	4	2 PU0140	carbon-monoxide de
38	6	17.1	4	2 I40697	biotin A - Citroba
39	6	17.1	4	2 A41890	protein D - Escher
40	6	17.1	4	2 T30569	hypothetical prote
41	6	17.1	4	2 T38888	COI intron 16 prot
42	6	17.1	4	2 A34626	RPGH-related neuro
43	6	17.1	4	2 A32480	achatin-I - giant
44	6	17.1	4	2 S39390	myosin-light-chain
45	6	17.1	4	2 PT0240	Ig heavy chain CRD

ALIGNMENTS

RESULT 1

B45525

actin I - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum

C:Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000

C:Accession: B45525

R:Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoenmaker, M.

Mol. Biochem. Parasitol. 35, 167-176, 1989

A:Title: Stage-specific expression and genomic organization of the actin genes of the mal

A:Reference number: A45525; MUID:89364996; PMID:2671721

A:Accession: B45525

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 <WES>

A:Cross-references: GB:J03988

A:Note: the authors translated the codon GAA for residue 3 as Gly

C:Comment: The actin I gene contains no introns.

Query Match 48.6%; Score 17; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GDC 5
Db 2 GEC 4

RESULT 2

S43959

Ig mu chain V region (clone 13) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999

C:Accession: S43959

R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;

Nucleic Acids Res. 22, 1389-1393, 1994

A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.

A:Reference number: S43956; MUID:94248036; PMID:8190629

A:Accession: S43959

A:Molecule type: DNA

A:Residues: 1-4 <WAG>

C:Keywords: immunoglobulin

Query Match 40.0%; Score 14; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRG 3
Db 2 CAG 4

RESULT 3

F22565

R-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)
 C:Species: Gastroclonium coulteri
 C>Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
 C:Accession: F22565
 R:Klotz, A.V.; Glazer, A.N.
 J. Biol. Chem. 260, 4856-4863, 1985
 A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
 A:Reference number: A22565; MUID:85182601; PMID:3886644
 A:Accession: F22565
 A:Molecule type: protein
 A:Residues: 1-5 <KLO>

Query Match 40.0%; Score 14; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDC 5
 DB 1 GTC 3

RESULT 4

PT0711
 T-cell receptor beta chain V-D-J region (120-20) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0607; PT0674; PT0678; PT0570; PT0711; PT0710
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0607
 A:Molecule type: not shown
 A:Status: translation not shown
 A:Residues: 1-4 <FE1>
 A:Experimental source: newborn thymus, strain BALB/c, 120-2J
 A:Accession: PT0674
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-4 <FE2>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
 A:Accession: PT0678
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-4 <FE3>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
 A:Accession: PT0570
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-4 <FE4>
 A:Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
 A:Accession: PT0711
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-4 <FE5>
 A:Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
 C:Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GD 4
 DB 3 GD 4

RESULT 5

PQ0689
 photosystem I 10, 4K H1 chain - common tobacco (fragment)
 C:Species: Nicotiana tabacum (common tobacco)
 C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999

C:Accession: PQ0689

R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiyura, M.
 Plant Physiol. 102, 1259-1267, 1993

A:Title: Molecular heterogeneity of photosystem I. psalD, psalE, psalF, psalH and psalL are a

A:Reference number: PQ0667; MUID:94105345; PMID:8278548

A:Accession: PQ0689

A:Molecule type: protein

A:Residues: 1-5 <O80>

C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 34.3%; Score 12; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GD 4
 DB 3 GD 4

RESULT 6

PT0513
 T-cell receptor beta chain V-D-J region (100-4AL) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0513; PT0606
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0513
 A:Molecule type: not shown
 A:Status: translation not shown
 A:Residues: 1-5 <FE2>
 A:Experimental source: adult thymus, strain BALB/c, clone 100-4AL
 A:Accession: PT0606
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <FE2>
 A:Experimental source: newborn thymus, strain BALB/c, clone 120-1S
 C:Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GD 4
 DB 3 GD 4

RESULT 7

PT0538
 T-cell receptor beta chain V-D-J region (126-1F) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0538; PT0539; PT0603
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0538
 A:Molecule type: not shown
 A:Status: translation not shown
 A:Residues: 1-5 <FE2>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F
 A:Accession: PT0539
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <FE3>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1H
 A:Accession: PT0603
 A:Status: translation not shown
 A:Molecule type: mRNA

A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AC
C;Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GD 4
||
Db 3 GD 4

RESULT 8

PT0703
T-cell receptor beta chain V-D-J region (135-1F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0703
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0703
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GD 4
||
Db 3 GD 4

RESULT 9

PT0690
T-cell receptor beta chain V-D-J region (140-1BD) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0690
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0690
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GD 4
||
Db 3 GD 4

RESULT 10

PT0573
T-cell receptor beta chain V-D-J region (141-1CC) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0573
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0573
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE2>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GD 4
||
Db 3 GD 4

RESULT 11

PT0679
T-cell receptor beta chain V-D-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0679; PT0708
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0679
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-2J
A;Accession: PT0708
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, 161-2B
C;Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GD 4
||
Db 3 GD 4

RESULT 12

S47552
ubiquitin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
C;Accession: S47552
R;Hubbard, M.J.; Carns, A.

Biochim. Biophys. Acta 1200, 191-196, 1994
A;Title: Differential feeding-related regulation of ubiquitin and calbindin(9kDa) in rat
A;Reference number: S47552; MUID:94304928; PMID:8031840

A;Accession: S47552
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <HUB>

Query Match 31.4%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RG 3
||
Db 2 RG 3

Job time : 39 secs

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RESULT 13
S5238
pallidipin - assassin bug (fragment)
C:Species: Triatoma pallidipennis (assassin bug)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000
C:Accession: S5238
R:Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleunin
Biochem. J. 307, 465-470, 1995
A:Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhibi
A:Reference number: S5238; MUID:95251610; PMID:7733884
A:Accession: S5238
A:Molecule type: protein
A:Residues: 1-4 <HAE>

Query Match          31.4%; Score 11; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DC 5
Db 2 EC 3

RESULT 14
A3382
cadmium-binding pentapeptide - downy thornapple
C:Species: Datura innoxia (downy thornapple)
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C:Accession: A3382
R:Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A:Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant c
A:Reference number: A94182; MUID:88016144; PMID:3477793
A:Accession: A3382
A:Molecule type: protein
A:Residues: 1-5 <JAC>

Query Match          31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DC 5
Db 1 EC 2

RESULT 15
PT0525
T-cell receptor beta chain V-D-J region (100-4J) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0525
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:9127601; PMID:1711558
A:Accession: PT0525
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match          31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RG 3
Db 3 RG 4
```

Search completed: September 22, 2004, 07:11:29